

References

- Kuloglu M, Ustundag B, Atmaca M, et al. Lipid peroxidation and antioxidant enzyme levels in patients with schizophrenia and bipolar disorder. *Cell Biochem Funct* 2002;20:171-5.
- Ranjekar PK, Hinge A, Hegde MV, et al. Decreased antioxidant enzymes and membrane essential polyunsaturated fatty acids in schizophrenic and bipolar mood disorder patients. *Psychiatry Res* 2003;121:109-22.
- Ozcan ME, Gulec M, Ozerol E, et al. Antioxidant enzyme activities and oxidative stress in affective disorders. *Int Clin Psychopharmacol* 2004;19:89-95.
- Ben-Shachar D. Mitochondrial dysfunction in schizophrenia: a possible linkage to dopamine. *J Neurochem* 2002;83:1241-51.
- Calabrese V, Scapagnini G, Giuffrida-Stella AM, et al. Mitochondrial involvement in brain function and dysfunction: relevance to aging, neurodegenerative disorders and longevity. *Neurochem Res* 2001;26:739-64.
- Floyd RA. Antioxidants, oxidative stress, and degenerative neurological disorders. *Proc Soc Exp Biol Med* 1999;222:236-45.
- Stork C, Renshaw PF. Mitochondrial dysfunction in bipolar disorder: evidence from magnetic resonance spectroscopy research. *Mol Psychiatry* 2005;10:900-19.
- Kato T, Kato N. Mitochondrial dysfunction in bipolar disorder. *Bipolar Disord* 2000;2:180-90.
- Konradi C, Eaton M, MacDonald ML, et al. Molecular evidence for mitochondrial dysfunction in bipolar disorder. *Arch Gen Psychiatry* 2004;61:300-8.
- Shao L, Young LT, Wang JF. Chronic treatment with mood stabilizers lithium and valproate prevents excitotoxicity by inhibiting oxidative stress in rat cerebral cortical cells. *Biol Psychiatry* 2005;58:879-84.
- Wang JF, Shao L, Sun X, et al. Glutathione S-transferase is a novel target for mood stabilizing drugs in primary cultured neurons. *J Neurochem* 2004;88:1477-84.
- Wang JF, Azzam JE, Young LT. Valproate inhibits oxidative damage to lipid and protein in primary cultured rat cerebrocortical cells. *Neuroscience* 2003;116:485-9.
- King TD, Jope RS. Inhibition of glycogen synthase kinase-3 protects cells from intrinsic but not extrinsic oxidative stress. *Neuroreport* 2005;16:597-601.
- Frey BN, Martins MR, Petronilho FC, et al. Increased oxidative stress after repeated amphetamine exposure: possible relevance as an animal model of acute mania. *Bipolar Disord* 2006;8:275-80.
- Dmitrzak-Weglarz M, Rybakowski JK, Slopian A, et al. Dopamine receptor D(1) gene -48A/G polymorphism is associated with bipolar illness but not with schizophrenia in a Polish population. *Neuropsychobiology* 2006;53:46-50.
- Greenwood TA, Schork NJ, Eskin E, et al. Identification of additional variants within the human dopamine transporter gene provides further evidence for an association with bipolar disorder in two independent samples. *Mol Psychiatry* 2006;11:125-33.
- Pantazopoulos H, Stone D, Walsh J, et al. Differences in the cellular distribution of D1 receptor mRNA in the hippocampus of bipolars and schizophrenics. *Synapse* 2004;54:147-53.
- Esterbauer H, Cheeseman KH. Determination of aldehydic lipid peroxidation products: malonaldehyde and 4-hydroxynonenal. *Methods Enzymol* 1990;186:407-21.
- Levine RL, Williams JA, Stadtman ER, et al. Carbonyl assays for determination of oxidatively modified proteins. *Methods Enzymol* 1994;233:346-57.
- Aebi H. Catalase in vitro. *Methods Enzymol* 1984;105:121-6.
- Bannister JV, Calabrese L. Assays for superoxide dismutase. *Methods Biochem Anal* 1987;32:279-312.
- Lowry OH, Rosebrough NJ, Farr AL, et al. Protein measurement with the Folin phenol reagent. *J Biol Chem* 1951;193:265-75.
- Frey BN, Andreazza AC, Ceresér KMM, et al. Effects of mood stabilizers on hippocampus BDNF levels in an animal model of mania. *Life Sci* 2006;79:281-6.
- Coyle JT, Manji HK. Getting balance: drugs for bipolar disorder share target. *Nat Med* 2002;8:557-8.
- Berman SB, Hastings TG. Dopamine oxidation alters mitochondrial respiration and induces permeability transition in brain mitochondria: implications for Parkinson's disease. *J Neurochem* 1999;73:1127-37.
- Burrows KB, Gudelsky G, Yamamoto BK. Rapid and transient inhibition of mitochondrial function following methamphetamine or 3,4-methylenedioxymethamphetamine administration. *Eur J Pharmacol* 2000;398:11-8.
- Sonsalla PK, Nicklas WJ, Heikkila RE. Role for excitatory amino acids in methamphetamine-induced nigrostriatal dopaminergic toxicity. *Science* 1989;243:398-400.
- Wang JF, Bown C, Young LT. Differential display PCR reveals novel targets for the mood-stabilizing drug valproate including the molecular chaperone GRP78. *Mol Pharmacol* 1999;55:521-7.
- Carli M, Morissette M, Hebert C, et al. Effects of a chronic lithium treatment on central dopamine neurotransmitters. *Biochem Pharmacol* 1997;54:391-7.
- Yatham LN, Liddle PF, Shiah IS, et al. PET study of [(18)F]6-fluoro-L-dopa uptake in neuroleptic- and mood-stabilizer-naïve first-episode nonpsychotic mania: effects of treatment with divalproex sodium. *Am J Psychiatry* 2002;159:768-74.
- D'Almeida V, Camarini R, Azzalis LA, et al. Antioxidant defense in rat brain after chronic treatment with anorectic drugs. *Toxicol Lett* 1995;81:101-5.
- Carvalho F, Fernandes E, Remiao F, et al. Adaptive response of antioxidant enzymes in different areas of rat brain after repeated d-amphetamine administration. *Addict Biol* 2001;6:213-21.
- Andrades M, Ritter C, Moreira JC, et al. Oxidative parameters differences during non-lethal and lethal sepsis development. *J Surg Res* 2005;125:68-72.
- Bonatto F, Polydoro M, Andrades ME, et al. Effect of protein malnutrition on redox state of the hippocampus of rat. *Brain Res* 2005;1042:17-22.
- Barichello T, Bonatto F, Feier G, et al. No evidence for oxidative damage in the hippocampus after acute and chronic electroshock in rats. *Brain Res* 2004;1014:177-83.

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Cys	Glu	Phe	Pro	Phe	Val	Pro	Val	Val	Asp	Gly	Ala	Phe	Leu	Asp	Glu
		355					360					365			
Thr	Pro	Gln	Arg	Ser	Leu	Ala	Ser	Gly	Arg	Phe	Lys	Lys	Thr	Glu	Ile
	370					375					380				
Leu	Thr	Gly	Ser	Asn	Thr	Glu	Glu	Gly	Tyr	Tyr	Phe	Ile	Ile	Tyr	Tyr
385					390					395					400
Leu	Thr	Glu	Leu	Leu	Arg	Lys	Glu	Glu	Gly	Val	Thr	Val	Thr	Arg	Glu
				405					410					415	
Glu	Phe	Leu	Gln	Ala	Val	Arg	Glu	Leu	Asn	Pro	Tyr	Val	Asn	Gly	Ala
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Ala	Arg	Gln	Ala	Ile	Val	Phe	Glu	Tyr	Thr	Asp	Trp	Thr	Glu	Pro	Asp
		435					440					445			
Asn	Pro	Asn	Ser	Asn	Arg	Asp	Ala	Leu	Asp	Lys	Met	Val	Gly	Asp	Tyr
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His	Phe	Thr	Cys	Asn	Val	Asn	Glu	Phe	Ala	Gln	Arg	Tyr	Ala	Glu	Glu
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<212> DNA
<213> Anopheles gambiae strain KISUMU
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aca Thr	ccg Pro 130	ccc Pro	aac Asn	agc Ser	tgc Cys	gtg Val 135	cag Gln	atc Ile	gtg Val	gac Asp	acc Thr 140	gtg Val	ttc Phe	ggc Gly	gac Asp	432
ttc Phe 145	ccg Pro	ggc Gly	gcg Ala	acc Thr	atg Met 150	tgg Trp	aac Asn	ccg Pro	aac Asn	acg Thr 155	ccc Pro	ctg Leu	tcc Ser	gag Glu	gac Asp 160	480
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gcc Ala	gtc Val	atg Met	ctg Leu 180	tgg Trp	atc Ile	ttc Phe	ggc Gly	ggc Gly 185	ggc Gly	ttc Phe	tac Tyr	tcc Ser	ggc Gly 190	acc Thr	gcc Ala	576
acc Thr	ctg Leu	gac Asp 195	gtg Val	tac Tyr	gac Asp	cac His	cgg Arg 200	gcg Ala	ctt Leu	gcg Ala	tgc Ser	gag Glu 205	gag Glu	aac Asn	gtg Val	624
atc Ile	gtg Val 210	gtg Val	tcg Ser	ctg Leu	cag Gln	tac Tyr 215	cgc Arg	gtg Val	gcc Ala	agt Ser	ctg Leu 220	ggc Gly	ttc Phe	ctg Leu	ttt Phe	672
ctc Leu 225	ggc Gly	acc Thr	ccg Pro	gaa Glu	gcg Ala 230	ccg Pro	ggc Gly	aac Asn	gcg Ala	gga Gly 235	ctg Leu	ttc Phe	gat Asp	cag Gln	aac Asn 240	720
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ccg Pro	tcg Ser	cggt Arg	gtg Val 260	aca Thr	ctg Leu	ttc Phe	ggc Gly	gag Glu 265	agt Ser	gcc Ala	ggt Gly	gcc Ala	gtc Val 270	tcg Ser	gtg Val	816
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atc Ile	ctg Leu 290	cag Gln	agc Ser	ggc Gly	tcg Ser	ccg Pro 295	acg Thr	gca Ala	ccg Pro	tgg Trp	gca Ala 300	ttg Leu	gta Val	tcg Ser	cggt Arg	912
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ccg Pro	cac His	gaa Glu	ccg Pro	agc Ser 325	aag Lys	ctg Leu	agc Ser	gat Asp	gcgt Ala 330	gtc Val	gag Glu	tgt Cys	ctg Leu	cggt Arg 335	ggc Gly	1008
aag Lys	gat Asp	ccg Pro	cac His 340	gtg Val	ctg Leu	gtc Val	aac Asn	aac Asn 345	gag Glu	tgg Trp	ggc Gly	acgt Thr	ctc Leu 350	ggc Gly	att Ile	1056
tgc Cys	gag Glu	ttc Phe 355	ccg Pro	ttc Phe	gtg Val	ccg Pro	gtg Val 360	gtc Val	gac Asp	ggt Gly	gcgt Ala	ttc Phe 365	ctg Leu	gac Asp	gag Glu	1104
acgt	ccgt	cag	cggt	tcgt	ctc	gcc	agc	gggt	cggt	ttc	aag	aag	acgt	gag	atc	1152

263365US0XPCT																
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gag Glu	ttc Phe	ctg Leu	cag Gln 420	gcg Ala	gtg Val	cgc Arg	gag Glu	ctc Leu 425	aac Asn	ccg Pro	tac Tyr	gtg Val	aac Asn 430	ggg Gly	gcg Ala	1296
gcc Ala	cgg Arg	cag Gln 435	gcg Ala	atc Ile	gtg Val	ttc Phe	gag Glu 440	tac Tyr	acc Thr	gac Asp	tgg Trp	acc Thr 445	gag Glu	ccg Pro	gac Asp	1344
aac Asn	ccg Pro 450	aac Asn	agc Ser	aac Asn	cgg Arg	gac Asp 455	gcg Ala	ctg Leu	gac Asp	aag Lys	atg Met 460	gtg Val	ggc Gly	gac Asp	tat Tyr	1392
cac His 465	ttc Phe	acc Thr	tgc Cys	aac Asn	gtg Val 470	aac Asn	gag Glu	ttc Phe	gcg Ala	cag Gln 475	cgg Arg	tac Tyr	gcc Ala	gag Glu	gag Glu 480	1440
ggc Gly	aac Asn	aac Asn	gtc Val	tac Tyr 485	atg Met	tat Tyr	ctg Leu	tac Tyr	acg Thr 490	cac His	cgc Arg	agc Ser	aaa Lys	ggc Gly 495	aac Asn	1488
ccg Pro	tgg Trp	ccg Pro	cgc Arg 500	tgg Trp	acg Thr	ggc Gly	gtg Val	atg Met 505	cac His	ggc Gly	gac Asp	gag Glu	atc Ile 510	aac Asn	tac Tyr	1536
gtg Val	ttc Phe	ggc Gly 515	gaa Glu	ccg Pro	ctc Leu	aac Asn	ccc Pro 520	acc Thr	ctc Leu	ggc Gly	tac Tyr 525	acc Thr 525	gag Glu	gac Asp	gag Glu	1584
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ccc Pro	aag Lys	cac His	acc Thr	gcc Ala 565	cac His	gga Gly	cgg Arg	cac His	tat Tyr 570	ctg Leu	gag Glu	ctg Leu	ggc Gly 575	ctc Leu 575	aac Asn	1728
acg Thr	tcc Ser	ttc Phe	gtc Val 580	ggt Gly	cgg Arg	ggc Gly	cca Pro	cgg Arg 585	ttg Leu	agg Arg	cag Gln	tgt Cys	gcc Ala 590	ttc Phe	tgg Trp	1776
aag Lys	aag Lys	tac Tyr 595	ctt Leu	ccc Pro	cag Gln	cta Leu	gtt Val 600	gca Ala	gct Ala	acc Thr	tcg Ser	aac Asn 605	cta Leu	cca Pro	ggg Gly	1824
cca Pro	gca Ala 610	ccg Pro	ccc Pro	agt Ser	gaa Glu	ccg Pro 615	tgc Cys	gaa Glu	agc Ser	agc Ser	gca Ala 620	ttt Phe	ttt Phe	tac Tyr	cga Arg	1872
cct Pro 625	gat Asp	ctg Leu	atc Ile	gtg Val	ctg Leu 630	ctg Leu	gtg Val	tcg Ser	ctg Leu	ctt Leu 635	acg Thr	gcg Ala	acc Thr	gtc Val	aga Arg 640	1920
ttc	ata	caa	taa													1932

Phe Ile Gln

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 <212> PRT
 <213> Anopheles gambiae strain KISUMU

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 35 40 45
 Gly Ala Thr Pro Arg Arg Arg Gly Leu Thr Arg Arg Glu Ser Asn Ser
 50 55 60
 Asp Ala Asn Asp Asn Asp Pro Leu Val Val Asn Thr Asp Lys Gly Arg
 65 70 75 80
 Ile Arg Gly Ile Thr Val Asp Ala Pro Ser Gly Lys Lys Val Asp Val
 85 90 95
 Trp Leu Gly Ile Pro Tyr Ala Gln Pro Pro Val Gly Pro Leu Arg Phe
 100 105 110
 Arg His Pro Arg Pro Ala Glu Lys Trp Thr Gly Val Leu Asn Thr Thr
 115 120 125
 Thr Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp
 130 135 140
 Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp
 145 150 155 160
 Cys Leu Tyr Ile Asn Val Val Ala Pro Arg Pro Arg Pro Lys Asn Ala
 165 170 175
 Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala
 180 185 190
 Thr Leu Asp Val Tyr Asp His Arg Ala Leu Ala Ser Glu Glu Asn Val
 195 200 205
 Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu Phe
 210 215 220
 Leu Gly Thr Pro Glu Ala Pro Gly Asn Ala Gly Leu Phe Asp Gln Asn
 225 230 235 240
 Leu Ala Leu Arg Trp Val Arg Asp Asn Ile His Arg Phe Gly Gly Asp
 245 250 255
 Pro Ser Arg Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Val Ser Val
 260 265 270
 Ser Leu His Leu Leu Ser Ala Leu Ser Arg Asp Leu Phe Gln Arg Ala
 275 280 285
 Ile Leu Gln Ser Gly Ser Pro Thr Ala Pro Trp Ala Leu Val Ser Arg
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 Glu Glu Ala Thr Leu Arg Ala Leu Arg Leu Ala Glu Ala Val Gly Cys

263365US0XPCT

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Lys	Asp	Pro	His ₃₄₀	Val	Leu	Val	Asn	Asn ₃₄₅	Glu	Trp	Gly	Thr	Leu ₃₅₀	Gly Ile
Cys	Glu	Phe ₃₅₅	Pro	Phe	Val	Pro	Val ₃₆₀	Val	Asp	Gly	Ala	Phe ₃₆₅	Leu	Asp Glu
Thr	Pro ₃₇₀	Gln	Arg	Ser	Leu	Ala ₃₇₅	Ser	Gly	Arg	Phe	Lys ₃₈₀	Lys	Thr	Glu Ile
Leu ₃₈₅	Thr	Gly	Ser	Asn	Thr ₃₉₀	Glu	Glu	Gly	Tyr	Tyr ₃₉₅	Phe	Ile	Ile	Tyr Tyr ₄₀₀
Leu	Thr	Glu	Leu	Leu ₄₀₅	Arg	Lys	Glu	Glu	Gly ₄₁₀	Val	Thr	Val	Thr	Arg ₄₁₅ Glu
Glu	Phe	Leu	Gln ₄₂₀	Ala	Val	Arg	Glu	Leu ₄₂₅	Asn	Pro	Tyr	Val	Asn ₄₃₀	Gly Ala
Ala	Arg	Gln ₄₃₅	Ala	Ile	Val	Phe	Glu ₄₄₀	Tyr	Thr	Asp	Trp	Thr ₄₄₅	Glu	Pro Asp
Asn	Pro ₄₅₀	Asn	Ser	Asn	Arg	Asp ₄₅₅	Ala	Leu	Asp	Lys	Met ₄₆₀	Val	Gly	Asp Tyr
His ₄₆₅	Phe	Thr	Cys	Asn	Val ₄₇₀	Asn	Glu	Phe	Ala	Gln ₄₇₅	Arg	Tyr	Ala	Glu Glu ₄₈₀
Gly	Asn	Asn	Val	Tyr ₄₈₅	Met	Tyr	Leu	Tyr	Thr ₄₉₀	His	Arg	Ser	Lys	Gly ₄₉₅ Asn
Pro	Trp	Pro	Arg ₅₀₀	Trp	Thr	Gly	Val	Met ₅₀₅	His	Gly	Asp	Glu	Ile ₅₁₀	Asn Tyr
Val	Phe	Gly	Glu	Pro	Leu	Asn	Pro	Thr	Leu	Gly	Tyr	Thr	Glu	Asp Glu
			515					520						525
Lys	Asp ₅₃₀	Phe	Ser	Arg	Lys	Ile ₅₃₅	Met	Arg	Tyr	Trp	Ser ₅₄₀	Asn	Phe	Ala Lys
Thr ₅₄₅	Gly	Asn	Pro	Asn	Pro ₅₅₀	Asn	Thr	Ala	Ser	Ser ₅₅₅	Glu	Phe	Pro	Glu Trp ₅₆₀
Pro	Lys	His	Thr	Ala ₅₆₅	His	Gly	Arg	His	Tyr ₅₇₀	Leu	Glu	Leu	Gly	Leu ₅₇₅ Asn
Thr	Ser	Phe	Val ₅₈₀	Gly	Arg	Gly	Pro	Arg ₅₈₅	Leu	Arg	Gln	Cys	Ala ₅₉₀	Phe Trp
Lys	Lys	Tyr ₅₉₅	Leu	Pro	Gln	Leu	Val ₆₀₀	Ala	Ala	Thr	Ser	Asn ₆₀₅	Leu	Pro Gly
Pro	Ala ₆₁₀	Pro	Pro	Ser	Glu	Pro ₆₁₅	Cys	Glu	Ser	Ser	Ala ₆₂₀	Phe	Phe	Tyr Arg
Pro ₆₂₅	Asp	Leu	Ile	Val	Leu ₆₃₀	Leu	Val	Ser	Leu	Leu ₆₃₅	Thr	Ala	Thr	Val Arg ₆₄₀
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 <213> Culex pipiens strain S-LAB

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 <212> PRT
 <213> Culex pipiens strain S-LAB

<400> 7

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 35 40 45
 Leu Gly Ser Lys Tyr Ser Gln Ser Ser Ser Leu Ser Ser Ser Ser Gln
 50 55 60
 Ser Ser Ser Ser Leu Ala Glu Glu Ala Thr Leu Asn Lys Asp Ser Asp
 65 70 75 80
 Ala Phe Phe Thr Pro Tyr Ile Gly His Gly Asp Ser Val Arg Ile Val
 85 90 95
 Asp Ala Glu Leu Gly Thr Leu Glu Arg Glu His Ile His Ser Thr Thr
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 Thr Arg Arg Arg Gly Leu Thr Arg Arg Glu Ser Ser Ser Asp Ala Thr
 115 120 125
 Asp Ser Asp Pro Leu Val Ile Thr Thr Asp Lys Gly Lys Ile Arg Gly
 130 135 140
 Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val Asp Ala Trp Met Gly
 145 150 155 160
 Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu Arg Phe Arg His Pro
 165 170 175
 Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn Ala Thr Lys Pro Pro
 180 185 190
 Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly
 195 200 205
 Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr
 210 215 220
 Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met
 225 230 235 240
 Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala Thr Leu Asp
 245 250 255
 Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu Asn Val Ile Val Val
 260 265 270
 Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu Phe Leu Gly Thr
 275 280 285
 Pro Glu Ala Pro Gly Asn Ala Gly Leu Phe Asp Gln Asn Leu Ala Leu
 290 295 300
 Arg Trp Val Arg Asp Asn Ile His Arg Phe Gly Gly Asp Pro Ser Arg
 305 310 315 320
 Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Val Ser Val Ser Leu His
 325 330 335
 Leu Leu Ser Ala Leu Ser Arg Asp Leu Phe Gln Arg Ala Ile Leu Gln
 340 345 350
 Ser Gly Ser Pro Thr Ala Pro Trp Ala Leu Val Ser Arg Glu Glu Ala
 355 360 365

263365US0XPCT

Thr Leu Arg Ala Leu Arg Leu Ala Glu Ala Val Asn Cys Pro His Asp
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 Pro Phe Val Pro Val Val Asp Gly Ala Phe Leu Asp Glu Thr Pro Gln
 420 425 430
 Arg Ser Leu Ala Ser Gly Arg Phe Lys Lys Thr Asp Ile Leu Thr Gly
 435 440 445
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 450 455 460
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 465 470 475 480
 Gln Ala Val Arg Glu Leu Asn Pro Tyr Val Asn Gly Ala Ala Arg Gln
 485 490 495
 Ala Ile Val Phe Glu Tyr Thr Asp Trp Ile Glu Pro Asp Asn Pro Asn
 500 505 510
 Ser Asn Arg Asp Ala Leu Asp Lys Met Val Gly Asp Tyr His Phe Thr
 515 520 525
 Cys Asn Val Asn Glu Phe Ala Gln Arg Tyr Ala Glu Glu Gly Asn Asn
 530 535 540
 Val Phe Met Tyr Leu Tyr Thr His Arg Ser Lys Gly Asn Pro Trp Pro
 545 550 555 560
 Arg Trp Thr Gly Val Met His Gly Asp Glu Ile Asn Tyr Val Phe Gly
 565 570 575
 Glu Pro Leu Asn Ser Ala Leu Gly Tyr Gln Asp Asp Glu Lys Asp Phe
 580 585 590
 Ser Arg Lys Ile Met Arg Tyr Trp Ser Asn Phe Ala Lys Thr Gly Asn
 595 600 605
 Pro Asn Pro Ser Thr Pro Ser Val Asp Leu Pro Glu Trp Pro Lys His
 610 615 620
 Thr Ala His Gly Arg His Tyr Leu Glu Leu Gly Leu Asn Thr Thr Phe
 625 630 635 640
 Val Gly Arg Gly Pro Arg Leu Arg Gln Cys Ala Phe Trp Lys Lys Tyr
 645 650 655
 Leu Pro Gln Leu Val Ala Ala Thr Ser Asn Leu Gln Val Thr Pro Ala
 660 665 670
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 690 695 700

<210> 8
 <211> 91

<212> PRT

<213> *Culex pipiens*

<400> 8

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 Tyr Ala Glu₃₅ Glu Gly Asn Asn Val₄₀ Phe Met Tyr Leu Tyr₄₅ Thr His Arg
 Ser Lys₅₀ Gly Asn Pro Trp Pro₅₅ Arg Trp Thr Gly Val₆₀ Met His Gly Asp
 Glu Ile Asn Tyr Val Phe₇₀ Gly Glu Pro Leu Asn₇₅ Ser Ala Leu Gly Tyr₈₀
 Gln Asp Asp Glu Lys₈₅ Asp Phe Ser Arg Lys₉₀ Ile

<210> 9

<211> 91

<212> PRT

<213> *Aedes aegypti*

<400> 9

Thr Glu Pro Glu Asn₅ Pro Asn Ser Asn Arg₁₀ Asp Ala Leu Asp Lys₁₅ Met
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 Tyr Ala Glu₃₅ Glu Gly Asn Asn Val₄₀ Tyr Met Tyr Leu Tyr₄₅ Thr His Arg
 Ser Lys₅₀ Gly Asn Pro Trp Pro₅₅ Arg Trp Thr Gly Val₆₀ Met His Gly Asp
 Glu Ile Asn Tyr Val Phe₇₀ Gly Glu Pro Leu Asn₇₅ Ser Asp Leu Gly Tyr₈₀
 Met Glu Asp Glu Lys₈₅ Asp Phe Ser Arg Lys₉₀ Ile

<210> 10

<211> 91

<212> PRT

<213> *Aedes albopictus*

<400> 10

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 Tyr Ala Glu₃₅ Glu Gly Asn Asn Val₄₀ Tyr Met Tyr Leu Tyr₄₅ Thr His Arg
 Ser Lys₅₀ Gly Asn Pro Trp Pro₅₅ Arg Trp Thr Gly Val₆₀ Met His Gly Asp

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Glu Ile Asn Tyr Val Phe Gly Glu Pro Leu Asn Ser Asp Leu Gly Tyr
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Met Asp Asp Glu Lys Asp Phe Ser Arg Lys Ile
 85 90

<210> 11
 <211> 91
 <212> PRT
 <213> Anopheles darlingi

<400> 11
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 35 40 45
 Ser Lys Gly Asn Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp
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 Glu Ile Asn Tyr Val Phe Gly Glu Pro Leu Asn Pro Thr Leu Gly Tyr
 65 70 75 80
 Thr Asp Asp Glu Lys Gly Phe Ser Arg Lys Ile
 85 90

<210> 12
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 <212> PRT
 <213> Anopheles sundaicus

<400> 12
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 35 40 45
 Ser Lys Gly Asn Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp
 50 55 60
 Glu Ile Asn Tyr Val Phe Gly Glu Pro Leu Asn Pro Thr Leu Gly Tyr
 65 70 75 80
 Thr Glu Asp Glu Lys Asp Phe Ser Arg Lys Ile
 85 90

<210> 13
 <211> 91
 <212> PRT
 <213> Anopheles minimus

<400> 13
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 35 40 45
 Ser Lys Gly Asn Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp
 50 55 60
 Glu Ile Asn Tyr Val Phe Gly Glu Pro Leu Asn Pro Ser Leu Gly Tyr
 65 70 75 80
 Thr Glu Asp Glu Lys Asp Phe Ser Arg Lys Ile
 85 90

<210> 14

<211> 91

<212> PRT

<213> Anopheles moucheti

<400> 14

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 35 40 45
 Ser Lys Gly Asn Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp
 50 55 60
 Glu Ile Asn Tyr Val Phe Gly Glu Pro Leu Asn Pro Ser Leu Gly Tyr
 65 70 75 80
 Thr Glu Asp Glu Lys Asp Phe Ser Arg Lys Ile
 85 90

<210> 15

<211> 91

<212> PRT

<213> Anopheles arabiensis

<400> 15

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 35 40 45
 Ser Lys Gly Asn Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp
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 65 70 75 80
 Thr Glu Asp Glu Lys Asp Phe Ser Arg Lys Ile
 85 90

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<210> 16
 <211> 91
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 <213> Anopheles funestus

<400> 16
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 35 40 45
 Ser Lys Gly Asn Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp
 50 55 60
 Glu Ile Asn Tyr Val Phe Gly Glu Pro Leu Asn Pro Ser Leu Gly Tyr
 65 70 75 80
 Thr Glu Asp Glu Lys Asp Phe Ser Arg Lys Ile
 85 90

<210> 17
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 <212> PRT
 <213> Anopheles pseudopunctipennis

<400> 17
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 35 40 45
 Ser Lys Gly Asn Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp
 50 55 60
 Glu Ile Asn Tyr Val Phe Gly Glu Pro Leu Asn Pro Gly Leu Gly Tyr
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 Thr Glu Asp Glu Lys Asp Phe Ser Arg Lys Ile
 85 90

<210> 18
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 <213> Anopheles sacharovi

<400> 18
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 20 25 30
 Tyr Ala Glu Glu Gly Asn Asn Val Tyr Met Tyr Leu Tyr Thr His Arg
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35

40

45

Ser Lys Gly Asn Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp
 50 55 60
 Glu Ile Asn Tyr Val Phe Gly Glu Pro Leu Asn Pro Ser Leu Gly Tyr
 65 70 75 80
 Thr Asp Asp Glu Lys Asp Phe Ser Arg Lys Ile
 85 90

<210> 19

<211> 91

<212> PRT

<213> Anopheles stephensi

<400> 19

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 20 25 30
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 35 40 45
 Ser Lys Gly Asn Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp
 50 55 60
 Glu Ile Asn Tyr Val Phe Gly Glu Pro Leu Asn Pro Ser Leu Gly Tyr
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 Thr Asp Asp Glu Lys Asp Phe Ser Arg Lys Ile
 85 90

<210> 20

<211> 91

<212> PRT

<213> Anopheles albimanus

<400> 20

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 35 40 45
 Ser Lys Gly Asn Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp
 50 55 60
 Glu Ile Asn Tyr Val Phe Gly Glu Pro Leu Asn Pro Thr Leu Gly Tyr
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 Thr Asp Asp Glu Lys Gly Phe Ser Arg Lys Ile
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<210> 21

<211> 91

<212> PRT

<213> Anopheles nili

<400> 21

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 35 40 45
 Ser Lys Gly Asn Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp
 50 55 60
 Glu Ile Asn Tyr Val Phe Gly Glu Pro Leu Asn Pro Ser Leu Gly Tyr
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 Thr Glu Asp Glu Lys Asp Phe Ser Arg Lys Met
 85 90

<210> 22

<211> 4209

<212> DNA

<213> Anopheles gambiae

<400> 22

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<212> DNA

<213> Anopheles gambiae strain KISUMU

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<213> Culex pipiens strain S-LAB

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<210> 26

<211> 273

<212> DNA

<213> Aedes aegypti

<400> 26

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tacatgtatc	tgtacactca	tagaagcaaa	ggtaaccctt	ggccacgggtg	gaccgggtgtg	180
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<210> 27

<211> 273

<212> DNA

<213> Aedes albopictus

<400> 27

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tacatgtatt	tgtacactca	cagaagcaaa	ggtaaccctt	ggccacgggtg	gaccgggggtg	180
atgcatgggtg	acgagatcaa	ctatgtattc	ggtgagccgt	tgaattccga	cctgggggtac	240
atggacgatg	agaaagattt	cagtagaaag	ata			273

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 tacatgtatc tgtacacgca ccgtagcaaa ggcaacccgt ggccccgctg gaccgggggtg 180
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 accgacgatg agaagggttt cagccggaag att 273

<210> 29
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 <213> *Anopheles sundaicus*

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 tacatgtatc tgtacacgca ccgaagcaaa ggcaacccgt ggccacgctg gaccgggtgtg 180
 atgcacgggtg acgagattaa ttacgtgttt ggagagccgc ttaacccac gctcggatac 240
 accgaggacg agaaggactt tagccggaag atc 273

<210> 30
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 <213> *Anopheles minimus*

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<210> 31
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 tacatgtacc tgtacacgca ccgaagcaaa ggcaacccgt ggccacgctg gaccggcggtt 180
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 accgaagacg agaaagactt tagccggaag atc 273

<210> 32
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 tacatgtatc tgtacacgca ccgcagcaaa ggcaacccgt ggccgcgctg gaccggcggtg 180
 atgcacggcg acgagatcaa ctacgtgttc ggcgaaccgc tcaacccac cctcggctac 240
 accgaggacg agaaagactt tagccggaag atc 273

<210> 33
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<212> DNA

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<400> 33

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tacatgtacc	tgtacacgca	ccgaagcaaa	ggcaacccat	ggccacgctg	gacgggctgt	180
atgcacgggtg	atgagattaa	ctatgtgttc	ggggaaccgc	tcaatcccag	cctcggctac	240
accgaggacg	agaaagactt	tagccggaag	atc			273

<210> 34

<211> 273

<212> DNA

<213> *Anopheles pseudopunctipennis*

<400> 34

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tacatgtatc	tgtacacgca	ccgaagcaaa	ggcaacccgt	ggccgcgctg	gaccggcgtc	180
atgcatgggg	acgagattaa	ctacgtgttt	ggggaaccgc	ttaacccggg	gctcggctat	240
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<210> 35

<211> 273

<212> DNA

<213> *Anopheles sacharovi*

<400> 35

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tacatgtacc	tgtacacgca	caggagcaaa	ggcaacccat	ggccgcgctg	gaccggcgtc	180
atgcatggcg	acgagatcaa	ctacgtgttc	ggcgaaccgc	tcaatcccag	cctaggctac	240
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<210> 36

<211> 273

<212> DNA

<213> *Anopheles stephensi*

<400> 36

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tacatgtatc	tgtacacgca	ccgaagcaaa	ggcaatccgt	ggccacgctg	gaccggcgtt	180
atgcatgggg	acgaaattaa	ctacgtgttc	ggggaaccgc	tcaaccctag	ccttgggtac	240
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<210> 37

<211> 273

<212> DNA

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tacatgtatc	tgtatacgca	ccgcagcaaa	ggcaatccgt	ggccccgttg	gacgggctgt	180
atgcatggcg	atgagatcaa	ctacgtgttt	ggtgaaccgc	tgaacccgac	gctcggctac	240
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<210> 38

<211> 273

<212> DNA

<213> *Anopheles nili*

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tacatgtacc tctacacgca ccggagcaaa ggcaatccct ggccgcgttg gacgggctgc 180
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accgaggacg agaaggactt cagccgcaag atg 273

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accamratca cgtytctcyc cgac 24

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<400> 48
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<213> Ciona intestinalis

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35 40 45
Glu Pro Asp Val Arg Gln Thr Thr Glu Phe Gly Asn Ser Cys Val Gln
50 55 60
Ile Asp Asp Glu Val Phe Gly Asn Phe Arg Glu Met Trp Asn Ala Pro
65 70 75 80
Asn Leu Lys Ser Glu Asp Cys Leu Tyr Leu Asn Ile Trp Thr Pro Arg
85 90 95
Ile Pro Thr Ser Thr Arg Ser Gln Pro Leu Ala Val Met Val Trp Ile
100 105 110
Tyr Gly Gly Ser Phe Tyr Ser Gly Thr Thr Ala Leu Ala Leu Tyr Asp
115 120 125
Gly Arg Tyr Leu Ala Ala Gln Gly Gly Val Val Val Val Ser Ile Asn
130 135 140
Tyr Arg Leu Gly Pro Leu Gly Phe Leu Ala Pro Leu Ala Gly Thr Pro
145 150 155 160
Gly Asn Ala Gly Leu Leu Asp Gln Gln Leu Ala Leu Lys Trp Val Arg
165 170 175
Asp Asn Ile Arg Ala Phe Gly Gly Asn Pro Asp Asn Val Thr Leu Met
180 185 190
Gly Glu Ser Ala Gly Ala Ala Ser Ile Gly Leu His Thr Val Ala Pro
195 200 205
Ser Ser Arg Gly Leu Phe Asn Arg Val Ile Phe Gln Ser Gly Asn Gln
210 215 220
Met Thr Pro Trp Ser Thr Ile Ser Leu Pro Thr Ser Leu Asn Arg Thr
225 230 235 240
Arg Ile Leu Ala Ala Asn Leu Arg Cys Pro Asn Pro Arg Thr Ser Ser
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245 250 255

Glu Leu Asp Val₂₆₀ Leu Thr Cys Leu Arg₂₆₅ Ser His Ser Ala Val₂₇₀ Asp Val

Phe Ser Asn₂₇₅ Ser Trp Ile Thr Gln₂₈₀ Glu Ile Phe Asp Phe₂₈₅ Pro Phe Val

Pro Val₂₉₀ His Gly Thr Ser Phe₂₉₅ Leu Pro Glu His Pro₃₀₀ His Glu Val Thr

Arg Lys Gly Glu Gln Ala₃₁₀ Asp Val Asp Val Met₃₁₅ Ala Gly His Asn Thr₃₂₀

Asn Glu Gly Ser Tyr₃₂₅ Phe Thr Leu Tyr Thr₃₃₀ Val Pro Gly Phe Asn₃₃₅ Ile

Ser Ser Gln Ser₃₄₀ Ile Leu Ser Lys Lys₃₄₅ Glu Tyr Ile Asp Gly₃₅₀ Ile Ala

Leu Ser Gly₃₅₅ Ile Lys Thr Asn Glu₃₆₀ Leu Gly Arg Ser Gly₃₆₅ Ala Ala Phe

Met Tyr₃₇₀ Ala Asp Trp Glu Asn₃₇₅ Pro Asp Asn Val Leu₃₈₀ Gln Tyr Arg Asp

Gly Val₃₈₅ Asn Glu Ile Val₃₉₀ Gly Asp Phe His Val₃₉₅ Val Cys Pro Thr Val₄₀₀

Leu Leu Thr Lys Arg₄₀₅ His Ser Arg Thr Phe₄₁₀ Ser Asn Asn Asn Val₄₁₅ Tyr

Leu Tyr His Leu₄₂₀ Ser Tyr Arg Leu Ser₄₂₅ Asn Asn Pro Trp Pro₄₃₀ Ala Trp

Met Gly Val₄₃₅ Met His Gly Tyr Glu₄₄₀ Ile Glu Leu Met Phe₄₄₅ Gly Thr Pro

Trp Phe₄₅₀ Gly Thr Ser Gln Phe₄₅₅ Thr Ser Gly Tyr Asn₄₆₀ Asp Val Asp Arg

Ser Val₄₆₅ Ser Arg Arg Met₄₇₀ Val His Tyr Trp Thr₄₇₅ Asn Phe Ala Lys Phe₄₈₀

Gly Asn Pro Asn Gly₄₈₅ Leu Arg Ser Ala Asn₄₉₀ Glu Leu Asp Leu Arg₄₉₅ Ser

Thr Asp Trp Pro₅₀₀ Arg Phe Asp Asp Val₅₀₅ Arg Gln Arg Tyr Leu₅₁₀ Glu Ile

Gly Ile Asp₅₁₅ Asp Asp Val Met Gly₅₂₀ Pro Phe Pro Asn Ser₅₂₅ Phe Arg Cys

Ala Phe₅₃₀ Trp Glu Arg Tyr Leu₅₃₅ Pro Ser Leu Lys Leu₅₄₀ Ala Ser Ser Ala

Asp Met₅₄₅ Asp Glu Val Glu₅₅₀ Thr Lys Trp Lys Ile₅₅₅ Glu Phe Asn Arg Trp₅₆₀

Thr Glu Ser Met Asp₅₆₅ Leu Trp Asp Arg Ser₅₇₀ Phe Lys Ala Tyr Ser₅₇₅ Lys

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<213> Ciona savignyi

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 35 40 45
 Pro Asp Val Lys Met Thr Ser Glu Phe Gly Asn Ser Cys Ile Gln Glu
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 65 70 75 80
 Ser Pro Asn Ala Lys Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Thr
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 Pro Val Arg Ser Arg His Ala Glu Pro Leu Ala Val Leu Val Trp Ile
 100 105 110
 Tyr Gly Gly Ser Tyr Tyr Ser Gly Thr Ser Ser Leu Ala Leu Tyr Asp
 115 120 125
 Gly Arg Tyr Leu Ala Ala Thr Gly Gly Val Val Val Val Ser Leu Asn
 130 135 140
 Tyr Arg Leu Gly Pro Ile Gly Phe Leu Ala Pro Leu Ala Asp Glu Thr
 145 150 155 160
 Pro Gly Asn Val Gly Leu Leu Asp Gln Gln Leu Ala Leu Lys Trp Val
 165 170 175
 Arg Asp Asn Ile Arg Glu Phe Gly Gly Asn Pro Asn Asn Val Thr Val
 180 185 190
 Met Gly Glu Ser Ala Gly Ala Ala Ser Ile Gly Leu His Thr Ile Ala
 195 200 205
 Pro Ser Ser Arg Gly Leu Phe Ser Arg Val Ile Leu Gln Ser Gly Asn
 210 215 220
 Gln Met Thr Pro Trp Ser Thr Ile Ser Leu Glu Thr Ser Leu Asn Arg
 225 230 235 240
 Thr Arg Thr Leu Ala Ala Asn Leu Asn Cys Pro Lys Pro Arg Thr Ala
 245 250 255
 Ser Glu Ala Asp Ile Leu Ala Cys Leu Arg Thr His Thr Ala Asn Glu
 260 265 270
 Val Phe Ala Gly Ser Trp Ile Thr Lys Glu Ile Phe Asp Phe Pro Phe
 275 280 285
 Val Pro Val His Gly Thr Thr Phe Leu Pro Glu His Pro His Glu Val
 290 295 300
 Thr Arg Arg Gly Asp Gln Ala Glu Val Asp Val Leu Ala Gly Tyr Asn
 305 310 315 320
 Thr Asn Glu Gly Ser Tyr Phe Thr Ile Tyr Thr Val Pro Gly Tyr Asn
 325 330 335

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Ile Thr Thr Asn Ser Val Leu Asn Arg Arg Gln Tyr Leu Ala Gly Val
340 345 350

Asp Leu Ser Gly Leu Lys Thr Asn Thr Met Gly Arg Ser Ala Ala Ala
355 360 365

Phe Met Tyr Thr Asp Trp Glu Asn Leu Asp Asn Glu Leu Gln Tyr Arg
370 375 380

Asp Ala Val Asn Glu Ile Val Gly Asp Phe His Val Val Cys Pro Thr
385 390 395 400

Val Leu Val Ser Lys Arg His Ser Asn Ser Phe Pro Asn Arg Asn Val
405 410 415

Phe Leu Tyr His Leu Ser Tyr Arg Val Ser Thr Asn Pro Trp Pro Ile
420 425 430

Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Leu Met Phe Gly Thr
435 440 445

Pro Trp Phe Gly Asn Ser Lys Phe Thr Arg Gly Tyr Ser Asp Leu Asp
450 455 460

Arg Ser Val Ser Arg Arg Met Val Arg Tyr Trp Thr Asn Phe Ala Lys
465 470 475 480

Phe Gly Asn Pro Asn Gly Leu Arg Asn Gln Asn Gln Glu Leu Val Ser
485 490 495

Asp Trp Pro Arg Phe Asn Asp Val Thr Gln Arg Tyr Leu Glu Ile Ala
500 505 510

Asp Asp Asp Val Thr Met Ala Pro Phe Pro Asp Ser Phe Arg Cys Ala
515 520 525

Phe Trp Gln Lys Tyr Leu Pro Ser Leu Gln Leu Ala Ser Ser Asn Met
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Asp Glu Val Glu Thr Lys Trp Lys Ile Glu Phe His Arg Trp Ser Glu
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35 40 45

Ser Thr Met Val Gln Gly Arg Glu Val His Val Phe Asn Gly Val Pro
50 55 60

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 Cys 100 Ile Gln Glu 100 Arg Tyr Glu Tyr Phe 105 Pro Gly Phe Ala Gly 110 Glu Glu
 Met 115 Trp Asn 115 Pro Asn Thr Asn Val 120 Ser Glu Asp Cys 125 Leu Tyr Leu Asn
 Ile 130 Trp Val Pro Thr Lys Thr 135 Arg Leu Arg His Gly 140 Arg Gly Leu Asn
 Phe 145 Gly Ser Asn Asp Tyr 150 Phe Gln Asp Asp 155 Asp Phe Gln Arg Gln 160
 His Gln Ser Lys Gly 165 Gly Leu Ala Met Leu 170 Val Trp Ile Tyr Gly 175 Gly
 Gly Phe Met Ser 180 Gly Thr Ser Thr Leu 185 Asp Ile Tyr Asn Ala 190 Glu Ile
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 Gly Ala 210 Phe Gly Phe Leu Tyr 215 Leu Ala Pro Tyr Ile 220 Asn Gly Tyr Glu
 Glu 225 Asp Ala Pro Gly Asn 230 Met Gly Met Trp Asp 235 Gln Ala Leu Ala Ile 240
 Arg Trp Leu Lys Glu 245 Asn Ala Lys Ala Phe 250 Gly Gly Asp Pro Asp 255 Leu
 Ile Thr Leu Phe 260 Gly Glu Ser Ala Gly 265 Gly Ser Ser Val Ser 270 Leu His
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 Ser Gly 290 Thr Leu Asn Ala Pro 295 Trp Ser His Met Thr 300 Ala Glu Lys Ala
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 Met Leu Lys Glu Ser 325 Pro Ser Thr Val Met 330 Gln Cys Met Arg Asn Val
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 Asp Pro 370 Met Thr Met Leu Arg 375 Glu Ala Asn Leu Glu 380 Gly Ile Asp Ile
 Leu 385 Val Gly Ser Asn Arg 390 Asp Glu Gly Thr Tyr 395 Phe Leu Leu Tyr Asp 400
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 Lys Phe Leu Glu 420 Ile Met Asn Thr Ile 425 Phe Asn Lys Ala Ser 430 Glu Pro

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 465 470 475 480
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 485 490 495
 Leu Trp Gly Glu Trp Met Gly Val Leu His Gly Asp Glu Val Glu Tyr
 500 505 510
 Ile Phe Gly Gln Pro Met Asn Ala Ser Leu Gln Tyr Arg Gln Arg Glu
 515 520 525
 Arg Asp Leu Ser Arg Arg Met Val Leu Ser Val Ser Glu Phe Ala Arg
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 580 585 590
 Trp Asn Asp Phe Leu Pro Arg Leu Arg Ala Trp Ser Val Pro Leu Lys
 595 600 605
 Asp Pro Cys Lys Leu Asp Asp His Thr Ser Ile Ala Ser Thr Ala Arg
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20

<210> 55
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19

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 Arg His Leu Ile Leu Cys Ser Leu Gly Leu Tyr Ser Ile Leu Val Gln
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 Ser Val His Cys Arg His His Asp Ile Gly Ser Ser Val Ala His Gln
 35 40 45
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 Ala Phe Phe Thr Pro Tyr Ile Gly His Gly Asp Ser Val Arg Ile Val
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 Asp Ala Glu Leu Gly Thr Leu Glu Arg Glu His Ile His Ser Thr Thr
 100 105 110
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 Thr Arg Arg Arg Gly Leu Thr Arg Arg Glu Ser Ser Ser Asp Ala Thr
 115 120 125
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 Asp Ser Asp Pro Leu Val Ile Thr Thr Asp Lys Gly Lys Ile Arg Gly
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 Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val Asp Ala Trp Met Gly
 145 150 155 160
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 Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu Arg Phe Arg His Pro
 165 170 175
 cga ccc gcc gaa aga tgg acc ggt gtg ctg aac gcg acc aaa cca ccc 576
 Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn Ala Thr Lys Pro Pro
 180 185 190
 aac tcc tgc gtc cag atc gtg gac acc gtg ttc ggt gac ttc ccg ggc 624
 Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly
 195 200 205
 gcg acc atg tgg aac ccg aac aca ccc ctc tcg gag gac tgt ctg tac 672
 Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr
 210 215 220
 atc aac gtg gtc gtg cca agg ccg agg ccc aag aat gcc gct gtc atg 720
 Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met
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500					505					510						
agc	aac	cgt	gac	gcg	ctc	gac	aag	atg	gtc	ggg	gat	tat	cac	ttc	acc	1584
Ser	Asn	Arg	Asp	Ala	Leu	Asp	Lys	Met	Val	Gly	Asp	Tyr	His	Phe	Thr	
		515					520					525				
tgc	aac	gtg	aac	gag	ttc	gcc	cag	cgg	tac	gcc	gag	gag	ggc	aac	aat	1632
Cys	Asn	Val	Asn	Glu	Phe	Ala	Gln	Arg	Tyr	Ala	Glu	Glu	Gly	Asn	Asn	
		530				535					540					
gtg	ttc	atg	tac	ctg	tac	acg	cac	aga	agc	aaa	gga	aat	ccc	tgg	ccg	1680
Val	Phe	Met	Tyr	Leu	Tyr	Thr	His	Arg	Ser	Lys	Gly	Asn	Pro	Trp	Pro	
					550					555					560	
agg	tgg	act	ggc	gtg	atg	cac	ggc	gac	gag	atc	aac	tac	gtg	ttt	ggc	1728
Arg	Trp	Thr	Gly	Val	Met	His	Gly	Asp	Glu	Ile	Asn	Tyr	Val	Phe	Gly	
				565					570					575		
gaa	ccg	ctg	aac	tcg	gcc	ctc	ggc	tac	cag	gac	gac	gag	aag	gac	ttt	1776
Glu	Pro	Leu	Asn	Ser	Ala	Leu	Gly	Tyr	Gln	Asp	Asp	Glu	Lys	Asp	Phe	
			580					585					590			
agc	cgg	aaa	att	atg	cga	tac	tgg	tcc	aac	ttt	gcc	aag	act	ggc	aat	1824
Ser	Arg	Lys	Ile	Met	Arg	Tyr	Trp	Ser	Asn	Phe	Ala	Lys	Thr	Gly	Asn	
		595					600					605				
cca	aac	ccg	agt	acg	ccg	agc	gtg	gac	ctg	ccc	gaa	tgg	ccc	aag	cac	1872
Pro	Asn	Pro	Ser	Thr	Pro	Ser	Val	Asp	Leu	Pro	Glu	Trp	Pro	Lys	His	
		610				615					620					
acc	gcc	cac	gga	cga	cac	tat	ctg	gag	ctg	gga	ctg	aac	acg	acc	ttc	1920
Thr	Ala	His	Gly	Arg	His	Tyr	Leu	Glu	Leu	Gly	Leu	Asn	Thr	Thr	Phe	
					630					635					640	
gtg	gga	cgg	ggc	cca	cga	ttg	cgg	cag	tgc	gct	ttc	tgg	aag	aaa	tat	1968
Val	Gly	Arg	Gly	Pro	Arg	Leu	Arg	Gln	Cys	Ala	Phe	Trp	Lys	Lys	Tyr	
				645					650					655		
ttg	ccg	caa	cta	gta	gca	gct	acc	tct	aac	ctc	caa	gta	act	ccc	gcg	2016
Leu	Pro	Gln	Leu	Val	Ala	Ala	Thr	Ser	Asn	Leu	Gln	Val	Thr	Pro	Ala	
			660					665					670			
cct	agc	gta	cct	tgc	gaa	agc	agc	tca	aca	tct	tat	cga	tcc	act	cta	2064
Pro	Ser	Val	Pro	Cys	Glu	Ser	Ser	Ser	Thr	Ser	Tyr	Arg	Ser	Thr	Leu	
		675				680						685				
ctt	cta	ata	gtc	aca	cta	ctt	tta	gta	acg	cgg	ttc	aag	att	taa		2109
Leu	Leu	Ile	Val	Thr	Leu	Leu	Leu	Val	Thr	Arg	Phe	Lys	Ile			
		690				695					700					

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<211> 702

<212> PRT

<213> Culex pipiens strain SR

<400> 57

Met Glu Ile Arg Gly Leu Ile Thr Arg Leu Leu Gly Pro Cys His Leu

1

5

10

15

Arg His Leu Ile Leu Cys Ser Leu Gly Leu Tyr Ser Ile Leu Val Gln

20

25

30

Ser Val His Cys Arg His His Asp Ile Gly Ser Ser Val Ala His Gln

35

40

45

Leu Gly Ser Lys Tyr Ser Gln Ser Ser Ser Leu Ser Ser Ser Ser Gln

50

55

60

263365US0XPCT

Ser₆₅ Ser Ser Ser Leu Ala₇₀ Glu Glu Ala Thr Leu₇₅ Asn Lys Asp Ser Asp₈₀
Ala Phe Phe Thr Pro₈₅ Tyr Ile Gly His Gly₉₀ Asp Ser Val Arg Ile₉₅ Val
Asp Ala Glu Leu₁₀₀ Gly Thr Leu Glu Arg₁₀₅ Glu His Ile His Ser₁₁₀ Thr Thr
Thr Arg Arg₁₁₅ Arg Gly Leu Thr Arg₁₂₀ Arg Glu Ser Ser Ser₁₂₅ Asp Ala Thr
Asp Ser₁₃₀ Asp Pro Leu Val Ile₁₃₅ Thr Thr Asp Lys Gly₁₄₀ Lys Ile Arg Gly
Thr Thr Leu Glu Ala Pro₁₅₀ Ser Gly Lys Lys Val₁₅₅ Asp Ala Trp Met Gly₁₆₀
Ile Pro Tyr Ala Gln₁₆₅ Pro Pro Leu Gly Pro₁₇₀ Leu Arg Phe Arg His₁₇₅ Pro
Arg Pro Ala Glu₁₈₀ Arg Trp Thr Gly Val₁₈₅ Leu Asn Ala Thr Lys₁₉₀ Pro Pro
Asn Ser Cys₁₉₅ Val Gln Ile Val Asp₂₀₀ Thr Val Phe Gly Asp₂₀₅ Phe Pro Gly
Ala Thr₂₁₀ Met Trp Asn Pro Asn₂₁₅ Thr Pro Leu Ser Glu₂₂₀ Asp Cys Leu Tyr
Ile₂₂₅ Asn Val Val Val Pro₂₃₀ Arg Pro Arg Pro Lys₂₃₅ Asn Ala Ala Val Met₂₄₀
Leu Trp Ile Phe Gly₂₄₅ Gly Ser Phe Tyr Ser₂₅₀ Gly Thr Ala Thr Leu₂₅₅ Asp
Val Tyr Asp His₂₆₀ Arg Thr Leu Ala Ser₂₆₅ Glu Glu Asn Val Ile₂₇₀ Val Val
Ser Leu Gln₂₇₅ Tyr Arg Val Ala Ser₂₈₀ Leu Gly Phe Leu Phe₂₈₅ Leu Gly Thr
Pro Glu₂₉₀ Ala Pro Gly Asn Ala₂₉₅ Gly Leu Phe Asp Gln₃₀₀ Asn Leu Ala Leu
Arg₃₀₅ Trp Val Arg Asp Asn₃₁₀ Ile His Arg Phe Gly₃₁₅ Gly Asp Pro Ser Arg₃₂₀
Val Thr Leu Phe Gly₃₂₅ Glu Ser Ala Gly Ala₃₃₀ Val Ser Val Ser Leu₃₃₅ His
Leu Leu Ser Ala₃₄₀ Leu Ser Arg Asp Leu₃₄₅ Phe Gln Arg Ala Ile₃₅₀ Leu Gln
Ser Gly Ser₃₅₅ Pro Thr Ala Pro Trp₃₆₀ Ala Leu Val Ser Arg₃₆₅ Glu Glu Ala
Thr Leu₃₇₀ Arg Ala Leu Arg Leu₃₇₅ Ala Glu Ala Val Asn₃₈₀ Cys Pro His Asp
Ala₃₈₅ Thr Lys Leu Ser Asp₃₉₀ Ala Val Glu Cys Leu₃₉₅ Arg Thr Lys Asp Pro₄₀₀
Asn Glu Leu Val Asp₄₀₅ Asn Glu Trp Gly Thr₄₁₀ Leu Gly Ile Cys Glu₄₁₅ Phe
Pro Phe Val Pro Val Val Asp Gly Ala Phe Leu Asp Glu Thr Pro Gln

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420	425	430
Arg Ser Leu Ala Ser Gly Arg Phe Lys Lys Thr Asp Ile Leu Thr Gly	440	445
Ser Asn Thr Glu Glu Gly Tyr Tyr Phe Ile Ile Tyr Tyr Leu Thr Glu	450	455
Leu Leu Arg Lys Glu Glu Gly Val Thr Val Thr Arg Glu Glu Phe Leu	465	470
Gln Ala Val Arg Glu Leu Asn Pro Tyr Val Asn Gly Ala Ala Arg Gln	485	490
Ala Ile Val Phe Glu Tyr Thr Asp Trp Ile Glu Pro Asp Asn Pro Asn	500	505
Ser Asn Arg Asp Ala Leu Asp Lys Met Val Gly Asp Tyr His Phe Thr	515	520
Cys Asn Val Asn Glu Phe Ala Gln Arg Tyr Ala Glu Glu Gly Asn Asn	530	535
Val Phe Met Tyr Leu Tyr Thr His Arg Ser Lys Gly Asn Pro Trp Pro	545	550
Arg Trp Thr Gly Val Met His Gly Asp Glu Ile Asn Tyr Val Phe Gly	565	570
Glu Pro Leu Asn Ser Ala Leu Gly Tyr Gln Asp Asp Glu Lys Asp Phe	580	585
Ser Arg Lys Ile Met Arg Tyr Trp Ser Asn Phe Ala Lys Thr Gly Asn	595	600
Pro Asn Pro Ser Thr Pro Ser Val Asp Leu Pro Glu Trp Pro Lys His	610	615
Thr Ala His Gly Arg His Tyr Leu Glu Leu Gly Leu Asn Thr Thr Phe	625	630
Val Gly Arg Gly Pro Arg Leu Arg Gln Cys Ala Phe Trp Lys Lys Tyr	645	650
Leu Pro Gln Leu Val Ala Ala Thr Ser Asn Leu Gln Val Thr Pro Ala	660	665
Pro Ser Val Pro Cys Glu Ser Ser Ser Thr Ser Tyr Arg Ser Thr Leu	675	680
Leu Leu Ile Val Thr Leu Leu Leu Val Thr Arg Phe Lys Ile	690	695
	700	

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 <213> Artificial Sequence

<220>
 <223> Synthetic DNA

<400> 58
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<211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic DNA

<400> 59
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<210> 60
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 <212> DNA
 <213> Culex pipiens pipiens strain Espro (R)

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 <222> (3)..(458)

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 Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys
 1 5 10 15

gtg gac gca tgg atg ggc att ccg tac gcg cag ccc ccg ctg ggt ccg 95
 Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro
 20 25 30

ctc cgg ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg ctg 143
 Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu
 35 40 45

aac gcg acc aaa cca ccc aac tcc tgc gtc cag atc gtg gac acc gtg 191
 Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val
 50 55 60

ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccc ctc 239
 Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu
 65 70 75

tcg gag gac tgt ctg tac atc aac gtg gtc gtg cca agg ccg agg ccc 287
 Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro
 80 85 90 95

aag aat gcc gct gtc atg ctg tgg atc ttt ggg ggt agc ttc tac tcc 335
 Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr Ser
 100 105 110

ggg act gcc acg ttg gac gtg tac gat cat cgg acg ctg gcc tcg gag 383
 Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu
 115 120 125

gag aac gtg atc gtg gtt tcg ctg cag tac cgt gtc gca agt ctt ggt 431
 Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly
 130 135 140

ttt ctc ttc ctg ggc aca ccg gag gca c 459
 Phe Leu Phe Leu Gly Thr Pro Glu Ala
 145 150

<210> 61
 <211> 461
 <212> DNA
 <213> Culex pipiens quinquefasciatus strain ProR(S)

<220>
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<222> (3)..(458)

<400> 61

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ac aag ggc aaa atc cgt gga acg aca ctg gaa gcg cct agt gga aag      47
  Lys Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys
    1          5          10
aag gtg gac gca tgg atg ggc att ccg tac gcg cag ccc ccg ctg ggt      95
  Lys Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly
                20          25          30
ccg ctc cgg ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg      143
  Pro Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val
                35          40          45
ctg aac gcg acc aaa ccg ccc aac tcc tgc gtc cag atc gtg gac acc      191
  Leu Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr
                50          55          60
gtg ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccg      239
  Val Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro
                65          70          75
ctc tcg gag gac tgt ctg tac atc aac gtg gtc gtg cca cgg ccc agg      287
  Leu Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg
    80          85          90          95
ccc aag aat gcc gcc gtc atg ctg tgg atc ttc ggg ggt ggc ttc tac      335
  Pro Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr
                100          105          110
tcc ggg act gcc acg ctg gac gtg tac gac cac cgg acg ctg gcc tcg      383
  Ser Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser
                115          120          125
gag gag aac gtg atc gta gtt tcg ctg cag tac cgt gtc gca agt ctt      431
  Glu Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu
                130          135          140
ggg ttt ctc ttc ctg ggc aca ccg gag gca                                461
  Gly Phe Leu Phe Leu Gly Thr Pro Glu
    145          150

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<210> 62

<211> 448

<212> DNA

<213> Culex pipiens pipiens strain S-LAB (S)

<220>

<221> CDS

<222> (3)..(446)

<400> 62

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    1          5          10
gtg gac gca tgg atg ggc att ccg tac gcg cag ccc ccg ctg ggt ccg      95
  Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro
                20          25          30
ctc cgg ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg ctg      143
  Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu
                35          40          45
aac gcg acc aaa ccg ccc aac tcc tgc gtc cag atc gtg gac acc gtg      191
  Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val
                50          55          60

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ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccg ctc Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu 65 70 75	239
tcg gag gac tgt ctg tac atc aac gtg gtc gtg cca cgg ccc agg ccc Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro 80 85 90 95	287
aag aat gcc gcc gtc atg ctg tgg atc ttc ggg ggt ggc ttc tac tcc Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser 100 105 110	335
ggg act gcc acg ctg gac gtg tac gac cac cgg acg ctg gcc tcg gag Gly Thr Ala Thr 115 Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu 120 125	383
gag aac gtg atc gta gtt tcg ctg cag tac cgt gtc gca agt ctt ggg Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly 130 135 140	431
ttt ctc ttc ctg ggc ac Phe Leu Phe Leu Gly 145	448
<210> 63	
<211> 459	
<212> DNA	
<213> Culex pipiens pipiens strain Padova (R)	
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<221> CDS	
<222> (3)..(458)	
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gtg gac gca tgg atg ggc att ccg tac gcg cag ccc ccg ctg ggt ccg Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro 20 25 30	95
ctc cgg ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg ctg Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu 35 40 45	143
aac gcg acc aaa cca ccc aac tcc tgc gtc cag atc gtg gac acc gtg Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val 50 55 60	191
ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccc ctc Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu 65 70 75	239
tcg gag gac tgt ctg tac atc aac gtg gtc gtg cca agg ccg agg ccc Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro 80 85 90 95	287
aag aat gcc gct gtc atg ctg tgg atc ttt ggg ggt agc ttc tac tcc Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr Ser 100 105 110	335
ggg act gcc acg ttg gac gtg tac gat cat cgg acg ctg gcc tcg gag Gly Thr Ala Thr 115 Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu 120 125	383
gag aac gtg atc gtg gtt tcg ctg cag tac cgt gtc gca agt ctt ggt Page 40	431

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Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly
130 135 140

ttt ctc ttc ctg ggc aca ccg gag gca c 459
Phe Leu Phe Leu Gly Thr Pro Glu Ala

145 150

<210> 64
<211> 463
<212> DNA
<213> Culex pipiens pipiens strain Praias (R)

<220>
<221> CDS
<222> (1)..(462)

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Asp Lys Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys
1 5 10 15

aag gtg gac gca tgg atg ggc att ccg tac gcg cag ccc ccg ctg ggt 96
Lys Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly
20 25 30

ccg ctc cgg ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg 144
Pro Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val
35 40 45

ctg aac gcg acc aaa cca ccc aac tcc tgc gtc cag atc gtg gac acc 192
Leu Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr
50 55 60

gtg ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccc 240
Val Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro
65 70 75 80

ctc tcg gag gac tgt ctg tac atc aac gtg gtc gtg cca agg ccg agg 288
Leu Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg
85 90 95

ccc aag aat gcc gct gtc atg ctg tgg atc ttt ggg ggt agc ttc tac 336
Pro Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr
100 105 110

tcc ggg act gcc acg ttg gac gtg tac gat cat cgg acg ctg gcc tcg 384
Ser Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser
115 120 125

gag gag aac gtg atc gtg gtt tcg ctg cag tac cgt gtc gca agt ctt 432
Glu Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu
130 135 140

ggt ttt ctc ttc ctg ggc aca ccg gag gca c 463
Gly Phe Leu Phe Leu Gly Thr Pro Glu Ala
145 150

<210> 65
<211> 463
<212> DNA
<213> Culex pipiens quinquefasciatus strain Supercar (R)

<220>
<221> CDS
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<400> 65

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 1 5 10 15
 aag gtg gac gca tgg atg ggc att ccg tac gcg cag ccc ccg ctg ggt 96
 Lys Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly
 20 25 30
 ccg ctc cgg ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg 144
 Pro Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val
 35 40 45
 ctg aac gcg acc aaa cca ccc aac tcc tgc gtc cag atc gtg gac acc 192
 Leu Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr
 50 55 60
 gtg ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccc 240
 Val Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro
 65 70 75 80
 ctc tcg gag gac tgt ctg tac atc aac gtg gtc gtg cca agg ccg agg 288
 Leu Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg
 85 90 95
 ccc aag aat gcc gct gtc atg ctg tgg atc ttt ggg ggt agc ttc tac 336
 Pro Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr
 100 105 110
 tcc ggg act gcc acg ttg gac gtg tac gat cat cgg acg ctg gcc tcg 384
 Ser Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser
 115 120 125
 gag gag aac gtg atc gtg gtt tcg ctg cag tac cgt gtc gca agt ctt 432
 Glu Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu
 130 135 140
 ggt ttt ctc ttc ctg ggc aca ccg gag gca c 463
 Gly Phe Leu Phe Leu Gly Thr Pro Glu Ala
 145 150

<210> 66

<211> 448

<212> DNA

<213> Culex pipiens pipiens strain Bruges A (S)

<220>

<221> CDS

<222> (3)..(446)

<400> 66

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 Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys
 1 5 10 15
 gtg gac gca tgg atg ggc att ccg tac gcg cag ccc ccg ctg ggt ccg 95
 Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro
 20 25 30
 ctc cgg ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg ctg 143
 Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu
 35 40 45
 aac gcg acc aaa cca ccc aac tcc tgc gtc cag atc gtg gac acc gtg 191
 Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val
 50 55 60
 ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccc ctc 239

263365US0XPCT

Phe	Gly	Asp	Phe	Pro	Gly	Ala	Thr	Met	Trp	Asn	Pro	Asn	Thr	Pro	Leu	
	65					70					75					
tcg	gag	gac	tgt	ctg	tac	atc	aac	gtg	gtc	gtg	cca	agg	ccg	agg	ccc	287
Ser	Glu	Asp	Cys	Leu	Tyr	Ile	Asn	Val	Val	Val	Pro	Arg	Pro	Arg	Pro	
	80				85					90					95	
aag	aat	gcc	gct	gtc	atg	ctg	tgg	atc	ttt	ggg	ggt	ggc	ttc	tac	tcc	335
Lys	Asn	Ala	Ala	Val	Met	Leu	Trp	Ile	Phe	Gly	Gly	Gly	Phe	Tyr	Ser	
				100					105					110		
ggg	act	gcc	acg	ttg	gac	gtg	tac	gat	cat	cgg	acg	ctg	gcc	tcg	gag	383
Gly	Thr	Ala	Thr	Leu	Asp	Val	Tyr	Asp	His	Arg	Thr	Leu	Ala	Ser	Glu	
			115					120					125			
gag	aac	gtg	atc	gtg	gtt	tcg	ctg	cag	tac	cgt	gtc	gca	agt	ctt	ggt	431
Glu	Asn	Val	Ile	Val	Val	Ser	Leu	Gln	Tyr	Arg	Val	Ala	Ser	Leu	Gly	
		130					135					140				
ttt	ctc	ttc	ctg	ggc	ac											448
Phe	Leu	Phe	Leu	Gly												
	145															
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Gly	Lys	Ile	Arg	Gly	Thr	Thr	Leu	Glu	Ala	Pro	Ser	Gly	Lys	Lys	Val	
	1			5					10					15		
gac	gca	tgg	atg	ggc	att	ccg	tac	gcg	cag	cct	ccg	ctg	ggt	ccg	ctc	96
Asp	Ala	Trp	Met	Gly	Ile	Pro	Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Pro	Leu	
			20					25					30			
cgg	ttt	cga	cat	ccg	cga	ccc	gcc	gaa	aga	tgg	acc	ggt	gtg	ctg	aac	144
Arg	Phe	Arg	His	Pro	Arg	Pro	Ala	Glu	Arg	Trp	Thr	Gly	Val	Leu	Asn	
		35					40					45				
gcg	acc	aaa	ccg	ccc	aac	tcc	tgc	gtc	cag	atc	gtg	gac	acc	gtg	ttc	192
Ala	Thr	Lys	Pro	Pro	Asn	Ser	Cys	Val	Gln	Ile	Val	Asp	Thr	Val	Phe	
	50					55					60					
ggt	gac	ttc	ccg	ggg	gcc	acc	atg	tgg	aac	ccg	aac	aca	ccg	ctc	tcg	240
Gly	Asp	Phe	Pro	Gly	Ala	Thr	Met	Trp	Asn	Pro	Asn	Thr	Pro	Leu	Ser	
	65				70					75					80	
gag	gac	tgt	ctg	tac	atc	aac	gtg	gtc	gtg	cca	cgg	ccc	agg	ccc	aag	288
Glu	Asp	Cys	Leu	Tyr	Ile	Asn	Val	Val	Val	Pro	Arg	Pro	Arg	Pro	Lys	
				85					90					95		
aat	gcc	gcc	gtc	atg	ctg	tgg	atc	ttc	ggg	ggt	agc	ttc	tac	tcc	ggg	336
Asn	Ala	Ala	Val	Met	Leu	Trp	Ile	Phe	Gly	Gly	Ser	Phe	Tyr	Ser	Gly	
			100					105					110			
act	gcc	acg	ctg	gac	gtg	tac	gac	cac	cgg	acg	ctg	gcc	tcg	gag	gag	384
Thr	Ala	Thr	Leu	Asp	Val	Tyr	Asp	His	Arg	Thr	Leu	Ala	Ser	Glu	Glu	
		115					120					125				
aac	gtg	atc	gta	gtt	tcg	ctg	cag	tac	cgt	gtc	gca	agt	ctt	ggt	ttt	432

263365US0XPCT

Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
130 135 140

ctc ttc ctg ggc aca ccg gag gca c 457
Leu Phe Leu Gly Thr Pro Glu Ala
145 150

<210> 68
<211> 447
<212> DNA
<213> Culex pipiens quinquefasciatus strain DJI (R)

<220>
<221> CDS
<222> (1)..(444)

<400> 68
ggc aaa atc cgt gga acg aca ctg gaa gcg cct agc gga aag aag gtg 48
Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val
1 5 10 15

gac gca tgg atg ggc att ccg tac gcg cag cct ccg ctg ggt ccg ctc 96
Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu
20 25 30

cgg ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg ctg aac 144
Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
35 40 45

gcg acc aaa ccg ccc aac tcc tgc gtc cag atc gtg gac acc gtg ttc 192
Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
50 55 60

ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccg ctc tcg 240
Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
65 70 75 80

gag gac tgt ctg tac atc aac gtg gtc gtg cca cgg ccc agg ccc aag 288
Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
85 90 95

aat gcc gcc gtc atg ctg tgg atc ttc ggg ggt agc ttc tac tcc ggg 336
Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr Ser Gly
100 105 110

act gcc acg ctg gac gtg tac gac cac cgg acg ctg gcc tcg gag gag 384
Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu
115 120 125

aac gtg atc gta gtt tcg ctg cag tac cgt gtc gca agt ctt ggt ttt 432
Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
130 135 140

ctc ttc ctg ggc aca 447
Leu Phe Leu Gly
145

<210> 69
<211> 457
<212> DNA
<213> Culex pipiens quinquefasciatus strain Harare (R)

<220>
<221> CDS
<222> (1)..(456)

<400> 69
ggc aaa atc cgt gga acg aca ctg gaa gcg cct agc gga aag aag gtg 48

263365US0XPCT

Gly	Lys	Ile	Arg	Gly	Thr	Thr	Leu	Glu	Ala	Pro	Ser	Gly	Lys	Lys	Val	
1				5					10					15		
gac	gca	tgg	atg	ggc	att	ccg	tac	gcg	cag	cct	ccg	ctg	ggt	ccg	ctc	96
Asp	Ala	Trp	Met	Gly	Ile	Pro	Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Pro	Leu	
			20					25					30			
cg	ttt	cga	cat	ccg	cga	ccc	gcc	gaa	aga	tgg	acc	ggt	gtg	ctg	aac	144
Arg	Phe	Arg	His	Pro	Arg	Pro	Ala	Glu	Arg	Trp	Thr	Gly	Val	Leu	Asn	
		35					40					45				
gcg	acc	aaa	ccg	ccc	aac	tcc	tgc	gtc	cag	atc	gtg	gac	acc	gtg	ttc	192
Ala	Thr	Lys	Pro	Pro	Asn	Ser	Cys	Val	Gln	Ile	Val	Asp	Thr	Val	Phe	
	50					55					60					
ggt	gac	ttc	ccg	ggg	gcc	acc	atg	tgg	aac	ccg	aac	aca	ccg	ctc	tcg	240
Gly	Asp	Phe	Pro	Gly	Ala	Thr	Met	Trp	Asn	Pro	Asn	Thr	Pro	Leu	Ser	
65				70					75						80	
gag	gac	tgt	ctg	tac	atc	aac	gtg	gtc	gtg	cca	cg	ccc	agg	ccc	aag	288
Glu	Asp	Cys	Leu	Tyr	Ile	Asn	Val	Val	Val	Pro	Arg	Pro	Arg	Pro	Lys	
			85					90					95			
aat	gcc	gcc	gtc	atg	ctg	tgg	atc	ttc	ggg	ggt	agc	ttc	tac	tcc	ggg	336
Asn	Ala	Ala	Val	Met	Leu	Trp	Ile	Phe	Gly	Gly	Ser	Phe	Tyr	Ser	Gly	
			100					105					110			
act	gcc	acg	ctg	gac	gtg	tac	gac	cac	cg	acg	ctg	gcc	tcg	gag	gag	384
Thr	Ala	Thr	Leu	Asp	Val	Tyr	Asp	His	Arg	Thr	Leu	Ala	Ser	Glu	Glu	
		115					120					125				
aac	gtg	atc	gta	gtt	tcg	ctg	cag	tac	cg	gtc	gca	agt	ctt	ggt	ttt	432
Asn	Val	Ile	Val	Val	Ser	Leu	Gln	Tyr	Arg	Val	Ala	Ser	Leu	Gly	Phe	
	130					135					140					
ctc	ttc	ctg	ggc	aca	ccg	gag	gca	c								457
Leu	Phe	Leu	Gly	Thr	Pro	Glu	Ala									
145					150											

<210> 70

<211> 458

<212> DNA

<213> Culex pipiens quinquefasciatus strain Martinique (R)

<220>

<221> CDS

<222> (1)..(456)

<400> 70

ggc	aaa	atc	cg	gga	acg	aca	ctg	gaa	gcg	cct	agc	gga	aag	aag	gtg	48
Gly	Lys	Ile	Arg	Gly	Thr	Thr	Leu	Glu	Ala	Pro	Ser	Gly	Lys	Lys	Val	
1				5					10					15		
gac	gca	tgg	atg	ggc	att	ccg	tac	gcg	cag	cct	ccg	ctg	ggt	ccg	ctc	96
Asp	Ala	Trp	Met	Gly	Ile	Pro	Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Pro	Leu	
			20					25					30			
cg	ttt	cga	cat	ccg	cga	ccc	gcc	gaa	aga	tgg	acc	ggt	gtg	ctg	aac	144
Arg	Phe	Arg	His	Pro	Arg	Pro	Ala	Glu	Arg	Trp	Thr	Gly	Val	Leu	Asn	
		35					40					45				
gcg	acc	aaa	ccg	ccc	aac	tcc	tgc	gtc	cag	atc	gtg	gac	acc	gtg	ttc	192
Ala	Thr	Lys	Pro	Pro	Asn	Ser	Cys	Val	Gln	Ile	Val	Asp	Thr	Val	Phe	
	50					55					60					
ggt	gac	ttc	ccg	ggg	gcc	acc	atg	tgg	aac	ccg	aac	aca	ccg	ctc	tcg	240
Gly	Asp	Phe	Pro	Gly	Ala	Thr	Met	Trp	Asn	Pro	Asn	Thr	Pro	Leu	Ser	
65				70					75						80	

263365US0XPCT

gag gac tgt ctg tac atc aac gtg gtc gtg cca cgg ccc agg ccc aag 288
 Glu Asp Cys Leu Tyr 85 Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys 95

 aat gcc gcc gtc atg ctg tgg atc ttc ggg ggt agc ttc tac tcc ggg 336
 Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr Ser Gly 100 105 110

 act gcc acg ctg gac gtg tac gac cac cgg acg ctg gcc tcg gag gag 384
 Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu 115 120 125

 aac gtg atc gta gtt tcg ctg cag tac cgt gtc gca agt ctt ggt ttt 432
 Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe 130 135 140

 ctc ttc ctg ggc aca ccg gag gca cc 458
 Leu Phe Leu Gly Thr Pro Glu Ala 145 150

 <210> 71
 <211> 447
 <212> DNA
 <213> Culex pipiens pipiens strain Barriol (R)

 <220>
 <221> CDS
 <222> (3)..(446)

 <400> 71
 ag ggc aaa atc cgt gga acg aca ctg gaa gcg cca agt gga aag aag 47
 Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys 1 5 10 15

 gtg gac gca tgg atg ggc att ccg tac gcg cag ccc ccg ctg ggt ccg 95
 Val Asp Ala Trp Met 20 Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro 25 30

 ctc cgg ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg ctg 143
 Leu Arg Phe Arg 35 His Pro Arg Pro Ala 40 Glu Arg Trp Thr Gly 45 Val Leu

 aac gcg acc aaa cca ccc aac tcc tgc gtc cag atc gtg gac acc gtg 191
 Asn Ala Thr 50 Lys Pro Pro Asn Ser 55 Cys Val Gln Ile Val 60 Asp Thr Val

 ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccc ctc 239
 Phe Gly 65 Asp Phe Pro Gly Ala 70 Thr Met Trp Asn Pro 75 Asn Thr Pro Leu

 tcg gag gac tgt ctg tac atc aac gtg gtc gtg cca agg ccg agg ccc 287
 Ser Glu Asp Cys Leu Tyr 85 Ile Asn Val Val Val Pro Arg Pro Arg Pro 80 90 95

 aag aat gcc gct gtc atg ctg tgg atc ttt ggg ggt agc ttc tac tcc 335
 Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr Ser 100 105 110

 ggg act gcc acg ttg gac gtg tac gat cat cgg acg ctg gcc tcg gag 383
 Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu 115 120 125

 gag aac gtg atc gtg gtt tcg ctg cag tac cgt gtc gca agt ctt ggt 431
 Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly 130 135 140

 ttt ctc ttc ctg ggc a 447

Phe Leu Phe Leu Gly
145

<210> 72

<211> 447

<212> DNA

<213> Culex pipiens pipiens strain Bleuete (S)

<220>

<221> CDS

<222> (3)..(446)

<400> 72

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ag ggc aaa atc cgt gga acg aca ctg gaa gcg cca agt gga aag aag      47
  Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys
    1          5          10
gtg gac gca tgg atg ggc att ccg tac gcg cag ccc ccg ctg ggt ccg      95
Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro
                20          25          30
ctc cgg ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg ctg      143
Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu
                35          40          45
aac gcg acc aaa cca ccc aac tcc tgc gtc cag atc gtg gac acc gtg      191
Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val
                50          55          60
ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccc ctc      239
Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu
    65          70          75
tcg gag gac tgt ctg tac atc aac gtg gtc gtg cca agg ccg agg ccc      287
Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro
    80          85          90
aag aat gcc gct gtc atg ctg tgg atc ttt ggg ggt ggc ttc tac tcc      335
Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser
                100          105          110
ggg act gcc acg ttg gac gtg tac gat cat cgg acg ctg gcc tcg gag      383
Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu
                115          120          125
gag aac gtg atc gtg gtt tcg ctg cag tac cgt gtc gca agt ctt ggt      431
Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly
                130          135          140
ttt ctc ttc ctg ggc a
Phe Leu Phe Leu Gly
    145

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<210> 73

<211> 448

<212> DNA

<213> Culex pipiens pipiens strain Bruges B (S)

<220>

<221> CDS

<222> (3)..(446)

<400> 73

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ag ggc aaa atc cgt gga acg aca ctg gaa gcg cca agt gga aag aag      47
  Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys
    1          5          10

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gtg	gac	gca	tgg	atg	ggc	att	ccg	tac	gcg	cag	ccc	ccg	ctg	ggt	ccg	95
Val	Asp	Ala	Trp	Met	Gly	Ile	Pro	Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Pro	
				20					25					30		
ctc	cgg	ttt	cga	cat	ccg	cga	ccc	gcc	gaa	aga	tgg	acc	ggt	gtg	ctg	143
Leu	Arg	Phe	Arg	His	Pro	Arg	Pro	Ala	Glu	Arg	Trp	Thr	Gly	Val	Leu	
			35					40					45			
aac	gcg	acc	aaa	cca	ccc	aac	tcc	tgc	gtc	cag	atc	gtg	gac	acc	gtg	191
Asn	Ala	Thr	Lys	Pro	Pro	Asn	Ser	Cys	Val	Gln	Ile	Val	Asp	Thr	Val	
		50					55					60				
ttc	ggt	gac	ttc	ccg	ggg	gcc	acc	atg	tgg	aac	ccg	aac	aca	ccc	ctc	239
Phe	Gly	Asp	Phe	Pro	Gly	Ala	Thr	Met	Trp	Asn	Pro	Asn	Thr	Pro	Leu	
	65					70					75					
tcg	gag	gac	tgt	ctg	tac	atc	aac	gtg	gtc	gtg	cca	agg	ccg	agg	ccc	287
Ser	Glu	Asp	Cys	Leu	Tyr	Ile	Asn	Val	Val	Val	Pro	Arg	Pro	Arg	Pro	
	80				85					90					95	
aag	aat	gcc	gct	gtc	atg	ctg	tgg	atc	ttt	ggg	ggt	ggc	ttc	tac	tcc	335
Lys	Asn	Ala	Ala	Val	Met	Leu	Trp	Ile	Phe	Gly	Gly	Gly	Phe	Tyr	Ser	
				100					105					110		
ggg	act	gcc	acg	ttg	gac	gtg	tac	gat	cat	cgg	acg	ctg	gcc	tcg	gag	383
Gly	Thr	Ala	Thr	Leu	Asp	Val	Tyr	Asp	His	Arg	Thr	Leu	Ala	Ser	Glu	
			115					120					125			
gag	aac	gtg	atc	gtg	gtt	tcg	ctg	cag	tac	cgt	gtc	gca	agt	ctt	ggt	431
Glu	Asn	Val	Ile	Val	Val	Ser	Leu	Gln	Tyr	Arg	Val	Ala	Ser	Leu	Gly	
		130					135					140				
ttt	ctc	ttc	ctg	ggc	ac											448
Phe	Leu	Phe	Leu	Gly												
	145															

<210> 74

<211> 447

<212> DNA

<213> Culex pipiens pipiens strain Heteren (S)

<220>

<221> CDS

<222> (3)..(446)

<400> 74

ag	ggc	aaa	atc	cgt	gga	acg	aca	ctg	gaa	gcg	cca	agt	gga	aag	aag	47
	Gly	Lys	Ile	Arg	Gly	Thr	Thr	Leu	Glu	Ala	Pro	Ser	Gly	Lys	Lys	
	1				5				10					15		

gtg	gac	gca	tgg	atg	ggc	att	ccg	tac	gcg	cag	ccc	ccg	ctg	ggt	ccg	95
Val	Asp	Ala	Trp	Met	Gly	Ile	Pro	Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Pro	
				20					25					30		

ctc	cgg	ttt	cga	cat	cca	cga	ccc	gcc	gaa	aga	tgg	acc	ggt	gtg	ctg	143
Leu	Arg	Phe	Arg	His	Pro	Arg	Pro	Ala	Glu	Arg	Trp	Thr	Gly	Val	Leu	
			35					40					45			

aac	gcg	acc	aaa	cca	ccc	aac	tcc	tgc	gtc	cag	atc	gtg	gac	aca	gtg	191
Asn	Ala	Thr	Lys	Pro	Pro	Asn	Ser	Cys	Val	Gln	Ile	Val	Asp	Thr	Val	
		50					55					60				

ttc	ggt	gac	ttc	ccg	ggg	gcc	acc	atg	tgg	aac	ccg	aac	aca	ccc	ctc	239
Phe	Gly	Asp	Phe	Pro	Gly	Ala	Thr	Met	Trp	Asn	Pro	Asn	Thr	Pro	Leu	
	65					70					75					

tcg	gag	gac	tgt	ctg	tac	atc	aac	gtg	gtc	gtg	cca	agg	ccg	agg	ccc	287
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

263365US0XPCT

Ser	Glu	Asp	Cys	Leu	Tyr	Ile	Asn	Val	Val	Val	Pro	Arg	Pro	Arg	Pro		
80					85					90					95		
aag	aat	gcc	gct	gtc	atg	ctg	tgg	atc	ttt	ggg	ggg	ggc	ttc	tac	tcc	335	
Lys	Asn	Ala	Ala	Val	Met	Leu	Trp	Ile	Phe	Gly	Gly	Gly	Phe	Tyr	Ser		
				100					105					110			
ggg	act	gcc	acg	ttg	gac	gtg	tac	gac	cat	cgg	acg	ctg	gcc	tcg	gaa	383	
Gly	Thr	Ala	Thr	Leu	Asp	Val	Tyr	Asp	His	Arg	Thr	Leu	Ala	Ser	Glu		
			115					120					125				
gag	aac	gtg	atc	gtg	gtt	tcg	ctg	cag	tac	cgt	gtc	gca	agt	ctt	ggg	431	
Glu	Asn	Val	Ile	Val	Val	Ser	Leu	Gln	Tyr	Arg	Val	Ala	Ser	Leu	Gly		
		130					135					140					
ttt	ctc	ttc	ctg	ggc	a											447	
Phe	Leu	Phe	Leu	Gly													
	145																
<210>	75																
<211>	450																
<212>	DNA																
<213>	Culex pipiens quinquefasciatus strain Ling (S)																
<220>																	
<221>	CDS																
<222>	(1)..(447)																
<400>	75																
cag	ggc	aaa	atc	cgt	gga	acg	aca	ctg	gaa	gcg	cct	agt	gga	aag	aag	48	
Gln	Gly	Lys	Ile	Arg	Gly	Thr	Thr	Leu	Glu	Ala	Pro	Ser	Gly	Lys	Lys		
	1			5					10					15			
gtg	gac	gcc	tgg	atg	ggc	att	ccg	tac	gcg	cag	ccc	ccg	ctg	ggg	ccg	96	
Val	Asp	Ala	Trp	Met	Gly	Ile	Pro	Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Pro		
			20					25					30				
ctc	cgg	ttt	cga	cat	ccg	cga	ccc	gcc	gaa	aga	tgg	acc	ggg	gtg	ctg	144	
Leu	Arg	Phe	Arg	His	Pro	Arg	Pro	Ala	Glu	Arg	Trp	Thr	Gly	Val	Leu		
		35					40					45					
aac	gcg	acc	aaa	ccg	ccc	aac	tcc	tgc	gtc	cag	atc	gtg	gac	acc	gtg	192	
Asn	Ala	Thr	Lys	Pro	Pro	Asn	Ser	Cys	Val	Gln	Ile	Val	Asp	Thr	Val		
	50					55					60						
ttc	ggg	gac	ttc	ccg	ggg	gcc	acc	atg	tgg	aac	ccg	aac	aca	ccg	ctc	240	
Phe	Gly	Asp	Phe	Pro	Gly	Ala	Thr	Met	Trp	Asn	Pro	Asn	Thr	Pro	Leu		
	65				70					75					80		
tcg	gag	gac	tgt	ctg	tac	atc	aac	gtg	gtc	gtg	cca	cgg	ccc	agg	ccc	288	
Ser	Glu	Asp	Cys	Leu	Tyr	Ile	Asn	Val	Val	Val	Pro	Arg	Pro	Arg	Pro		
				85					90					95			
aag	aat	gcc	gcc	gtc	atg	ctg	tgg	atc	ttc	ggg	ggg	ggc	ttc	tac	tcc	336	
Lys	Asn	Ala	Ala	Val	Met	Leu	Trp	Ile	Phe	Gly	Gly	Gly	Phe	Tyr	Ser		
			100					105					110				
ggg	act	gcc	acg	ctg	gac	gtg	tat	gac	cac	cgg	acg	ctg	gcc	tcg	gag	384	
Gly	Thr	Ala	Thr	Leu	Asp	Val	Tyr	Asp	His	Arg	Thr	Leu	Ala	Ser	Glu		
			115				120					125					
gag	aac	gtg	atc	gta	gtt	tcg	ctg	cag	tac	cgt	gtc	gca	agt	ctt	ggg	432	
Glu	Asn	Val	Ile	Val	Val	Ser	Leu	Gln	Tyr	Arg	Val	Ala	Ser	Leu	Gly		
	130					135					140						
ttt	ctc	ttc	ctg	ggc	aca											450	
Phe	Leu	Phe	Leu	Gly													

145

<210> 76
 <211> 448
 <212> DNA
 <213> *Culex pipiens quinquefasciatus* strain Mao (S)

<220>
 <221> CDS
 <222> (3)..(446)

<400> 76
 ac ggc aaa atc cgt gga acg aca ctg gaa gcg cct agt gga aag aag 47
 Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys
 1 5 10 15
 gtg gac gca tgg atg ggc att ccg tac gcg cag ccc ccg ctg ggt ccg 95
 Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro
 20 25 30
 ctc cgg ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg ctg 143
 Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu
 35 40 45
 aac gcg acc aaa ccg ccc aac tcc tgc gtc cag atc gtg gac acc gtg 191
 Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val
 50 55 60
 ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccg ctc 239
 Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu
 65 70 75
 tcg gag gac tgt ctg tac atc aac gtg gtc gtg cca cgg ccc agg ccc 287
 Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro
 80 85 90 95
 aag aat gcc gcc gtc atg ctg tgg atc ttc ggg ggt ggc ttc tac tcc 335
 Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser
 100 105 110
 ggg act gcc acg ctg gac gtg tac gac cac cgg acg ctg gcc tcg gag 383
 Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu
 115 120 125
 gag aac gtg atc gta gtt tcg ctg cag tac cgt gtc gca agt ctt ggt 431
 Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly
 130 135 140
 ttt ctc ttc ctg ggc ac 448
 Phe Leu Phe Leu Gly
 145

<210> 77
 <211> 433
 <212> DNA
 <213> *Culex pipiens quinquefasciatus* strain TemR (S)

<220>
 <221> CDS
 <222> (1)..(432)

<400> 77
 aaa atc cgt gga acg aca ctg gaa gcg cct agt gga aag aag gtg gac 48
 Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val Asp
 1 5 10 15
 gca tgg atg ggc att ccg tac gcg cag cct ccg ctg ggt ccg ctc cgg 96
 Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu Arg
 20 25 30
 Page 50

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20	25	30	
ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg ctg aac gcg Phe Arg His 35 Pro Arg Pro Ala Glu 40 Arg Trp Thr Gly Val 45 Leu Asn Ala			144
acc aaa cca ccc aac tcc tgc gtc cag atc gtg gac acc gtg ttc ggt Thr Lys 50 Pro Pro Asn Ser Cys 55 Val Gln Ile Val Asp 60 Thr Val Phe Gly			192
gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccg ctc tcg gag Asp 65 Phe Pro Gly Ala Thr 70 Met Trp Asn Pro Asn 75 Thr Pro Leu Ser Glu 80			240
gac tgt ctg tac atc aac gtg gtc gtg cca cgg ccc agg ccc aag aat Asp Cys Leu Tyr 85 Asn Val Val Val Pro 90 Arg Pro Arg Pro Lys 95 Asn			288
gcc gcc gtc atg ctg tgg atc ttc ggg ggt ggc ttc tac tcc ggg act Ala Ala Val Met 100 Leu Trp Ile Phe Gly 105 Gly Gly Phe Tyr Ser 110 Gly Thr			336
gcc acg ctg gac gtg tac gac cac cgg acg ctg acc tcg gag gag aac Ala Thr 115 Leu Asp Val Tyr Asp His 120 Arg Thr Leu Thr Ser 125 Glu Glu Asn			384
gtg atc gta gtt tcg ctg cag tac cgt gtc gca agt ctt ggt ttt ctc t Val Ile Val Val Ser Leu 135 Gln Tyr Arg Val Ala Ser 140 Leu Gly Phe Leu			433

<210> 78

<211> 448

<212> DNA

<213> Culex torrentium strain Uppsala

<220>

<221> CDS

<222> (3)..(446)

<400> 78

ag ggc aaa atc cgt gga acg aca ctg gaa gcg cca agt gga aag aag Gly Lys Ile Arg Gly 5 Thr Thr Leu Glu 10 Ala Pro Ser Gly Lys 15 Lys			47
gtg gac gca tgg atg ggc att ccg tac gcg cag cct ccg ctg ggt ccg Val Asp Ala Trp Met 20 Gly Ile Pro Tyr Ala 25 Gln Pro Pro Leu Gly 30 Pro			95
ctt cgg ttt cga cat cca cga ccc gcc gaa aga tgg acc ggt gtg ctg Leu Arg Phe Arg His 35 Pro Arg Pro Ala Glu Arg Trp Thr Gly Val 45 Leu			143
aac gcg acc aaa cca ccc aac tcc tgc gtc cag atc gtc gac acc gtg Asn Ala Thr 50 Lys Pro Pro Asn Ser 55 Cys Val Gln Ile Val 60 Asp Thr Val			191
ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccc ctc Phe Gly 65 Asp Phe Pro Gly 70 Ala Thr Met Trp Asn Pro 75 Asn Thr Pro Leu			239
tcg gaa gac tgt ctg tac atc aac gtt gtg gtg cca cgg ccg agg ccc Ser 80 Glu Asp Cys Leu Tyr 85 Ile Asn Val Val 90 Pro Arg Pro Arg Pro 95			287
aag aat gcc gcc gtc atg ctg tgg atc ttc ggg ggt gga ttc tac tcc Lys Asn Ala Ala Val 100 Met Leu Trp Ile Phe 105 Gly Gly Gly Phe 110 Tyr Ser			335

263365US0XPCT

ggg acc gcc acg ctg gac gtg tac gac cac cgg acg ctg gcc tcg gag 383
 Gly Thr Ala Thr 115 Leu Asp Val Tyr Asp 120 His Arg Thr Leu Ala Ser Glu
 gag aac gtg atc gtg gtt tcg ctg cag tac cgt gtc gca agt ctt ggt 431
 Glu Asn Val 130 Ile Val Val Ser Leu 135 Gln Tyr Arg Val Ala 140 Ser Leu Gly
 ttt ctc ttc ctg ggc ac 448
 Phe Leu Phe Leu Gly 145

<210> 79
 <211> 448
 <212> DNA
 <213> Culex pipiens quinquefasciatus strain Trans (S)

<220>
 <221> CDS

<222> (3)..(446)

<400> 79
 ag ggc aaa atc cgt gga acg aca ctg gaa gcg cct agt gga aag aag 47
 Gly Lys Ile Arg Gly 5 Thr Thr Leu Glu Ala 10 Pro Ser Gly Lys Lys 15
 gtg gac gca tgg atg ggc att ccg tac gcg cag cct ccg ctg ggt ccg 95
 Val Asp Ala Trp Met 20 Gly Ile Pro Tyr Ala 25 Gln Pro Pro Leu Gly 30 Pro
 ctc cgg ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg ctg 143
 Leu Arg Phe Arg 35 His Pro Arg Pro Ala 40 Glu Arg Trp Thr Gly 45 Val Leu
 aac gcg acc aaa cca ccc aac tcc tgc gtc cag atc gtg gac acc gtg 191
 Asn Ala Thr 50 Lys Pro Pro Asn Ser 55 Cys Val Gln Ile Val Asp Thr Val
 ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccg ctc 239
 Phe Gly 65 Asp Phe Pro Gly 70 Ala Thr Met Trp Asn Pro Asn Thr Pro Leu
 tcg gag gac tgt ctg tac atc aac gtg gtc gtg cca cgg ccc agg ccc 287
 Ser 80 Glu Asp Cys Leu Tyr 85 Ile Asn Val Val 90 Pro Arg Pro Arg Pro 95
 aag aat gcc gcc gtc atg ctg tgg atc ttc ggg ggt ggc ttc tac tcc 335
 Lys Asn Ala Ala Val 100 Met Leu Trp Ile Phe 105 Gly Gly Gly Phe Tyr Ser 110
 ggg act gcc acg ctg gac gtg tac gac cac cgg acg ctg acc tcg gag 383
 Gly Thr Ala Thr 115 Leu Asp Val Tyr Asp 120 His Arg Thr Leu Thr 125 Ser Glu
 gag aac gtg atc gta gtt tcg ctg cag tac cgt gtc gca agt ctt ggt 431
 Glu Asn Val 130 Ile Val Val Ser Leu 135 Gln Tyr Arg Val Ala 140 Ser Leu Gly
 ttt ctc ttc ctg ggc ac 448
 Phe Leu Phe Leu Gly 145

<210> 80
 <211> 412
 <212> DNA
 <213> Culex pipiens quinquefasciatus strain BED (S)

<220>

<221> CDS

<222> (1)..(411)

<400> 80

aca	ctg	gaa	gcg	cct	agt	gga	aag	aag	gtg	gac	gca	tgg	atg	ggc	att	48
Thr	Leu	Glu	Ala	Pro	Ser	Gly	Lys	Lys	Val	Asp	Ala	Trp	Met	Gly	Ile	
1				5					10					15		
ccg	tac	gcg	cag	cct	ccg	ctg	ggt	ccg	ctc	cgg	ttt	cga	cat	ccg	cga	96
Pro	Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Pro	Leu	Arg	Phe	Arg	His	Pro	Arg	
			20					25					30			
ccc	gcc	gaa	aga	tgg	acc	ggt	gtg	ctg	aac	gcg	acc	aaa	cca	ccc	aac	144
Pro	Ala	Glu	Arg	Trp	Thr	Gly	Val	Leu	Asn	Ala	Thr	Lys	Pro	Pro	Asn	
		35					40					45				
tcc	tgc	gtc	cag	atc	gtg	gac	acc	gtg	ttc	ggt	gac	ttc	ccg	ggg	gcc	192
Ser	Cys	Val	Gln	Ile	Val	Asp	Thr	Val	Phe	Gly	Asp	Phe	Pro	Gly	Ala	
	50					55					60					
acc	atg	tgg	aac	ccg	aac	aca	ccg	ctc	tcg	gag	gac	tgt	ctg	tac	atc	240
Thr	Met	Trp	Asn	Pro	Asn	Thr	Pro	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Ile	
65					70					75					80	
aac	gtg	gtc	gtg	cca	cgg	ccc	agg	ccc	aag	aat	gcc	gcc	gtc	atg	ctg	288
Asn	Val	Val	Val	Pro	Arg	Pro	Arg	Pro	Lys	Asn	Ala	Ala	Val	Met	Leu	
				85					90					95		
tgg	atc	ttc	ggg	ggt	ggc	ttc	tac	tcc	ggg	act	gcc	acg	ctg	gac	gtg	336
Trp	Ile	Phe	Gly	Gly	Gly	Phe	Tyr	Ser	Gly	Thr	Ala	Thr	Leu	Asp	Val	
			100					105					110			
tac	gac	cac	cgg	acg	ctg	gcc	tcg	gag	gag	aac	gtg	atc	gta	gtt	tcg	384
Tyr	Asp	His	Arg	Thr	Leu	Ala	Ser	Glu	Glu	Asn	Val	Ile	Val	Val	Ser	
		115					120					125				
ctg	cag	tac	cgt	gtc	gca	agt	ctt	ggt	t							412
Leu	Gln	Tyr	Arg	Val	Ala	Ser	Leu	Gly								
	130					135										

<210> 81

<211> 437

<212> DNA

<213> Culex pipiens quinquefasciatus strain BSQ (S)

<220>

<221> CDS

<222> (3)..(434)

<400> 81

ag	ggc	aaa	atc	cgt	gga	acg	aca	ctg	gaa	gcg	cct	agt	gga	aag	aag	47
	Gly	Lys	Ile	Arg	Gly	Thr	Thr	Leu	Glu	Ala	Pro	Ser	Gly	Lys	Lys	
	1				5				10					15		
gtg	gac	gcc	tgg	atg	ggc	att	ccg	tac	gcg	cag	ccc	ccg	ctg	ggt	ccg	95
Val	Asp	Ala	Trp	Met	Gly	Ile	Pro	Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Pro	
				20					25					30		
ctc	cgg	ttt	cga	cat	ccg	cga	ccc	gcc	gaa	aga	tgg	acc	ggt	gtg	ctg	143
Leu	Arg	Phe	Arg	His	Pro	Arg	Pro	Ala	Glu	Arg	Trp	Thr	Gly	Val	Leu	
			35					40					45			
aac	gcg	acc	aaa	ccg	ccc	aac	tcc	tgc	gtc	cag	atc	gtg	gac	acc	gtg	191
Asn	Ala	Thr	Lys	Pro	Pro	Asn	Ser	Cys	Val	Gln	Ile	Val	Asp	Thr	Val	
		50					55					60				

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ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccg ctc	239
Phe Gly 65 Asp Phe Pro Gly 70 Ala Thr Met Trp Asn Pro 75 Asn Thr Pro Leu	
tcg gag gac tgt ctg tac atc aac gtg gtc gtg cca cgg ccc agg ccc	287
Ser 80 Glu Asp Cys Leu Tyr 85 Ile Asn Val Val Val 90 Pro Arg Pro Arg Pro 95	
aag aat gcc gcc gtc atg ctg tgg atc ttc ggg ggt ggc ttc tac tcc	335
Lys Asn Ala Ala Thr 100 Met Leu Trp Ile Phe 105 Gly Gly Gly Phe Tyr 110 Ser	
ggg act gcc acg ctg gac gtg tac gac cac cgg acg ctg gcc tcg gag	383
Gly Thr Ala Thr 115 Leu Asp Val Tyr Asp 120 His Arg Thr Leu 125 Ala Ser Glu	
gag aac gtg atc gta gtt tcg ctg cag tac cgt gtc gca agt ctt ggg	431
Glu Asn Val 130 Ile Val Val Ser Leu 135 Gln Tyr Arg Val 140 Ala Ser Leu Gly	
ttt ctc	437
Phe	
<210> 82	
<211> 414	
<212> DNA	
<213> Culex pipiens quinquefasciatus strain Brazza (S)	
<220>	
<221> CDS	
<222> (2)..(412)	
<400> 82	
a ctg gaa gcg cct agt gga aag aag gtg gac gcc tgg atg ggc att ccg	49
Leu 1 Glu Ala Pro Ser 5 Gly Lys Lys Val 10 Asp Ala Trp Met Gly 15 Ile Pro	
tac gcg cag ccc ccg ctg ggt ccg ctc cgg ttt cga cat ccg cga ccc	97
Tyr Ala Gln Pro 20 Pro Leu Gly Pro Leu 25 Arg Phe Arg His Pro 30 Arg Pro	
gcc gaa aga tgg acc ggt gtg ctg aac gcg acc aaa ccg ccc aac tcc	145
Ala Glu Arg 35 Trp Thr Gly Val Leu 40 Asn Ala Thr Lys Pro 45 Pro Asn Ser	
tgc gtc cag atc gtg gac acc gtg ttc ggt gac ttc ccg ggg gcc acc	193
Cys Val 50 Gln Ile Val Asp Thr 55 Val Phe Gly Asp Phe 60 Pro Gly Ala Thr	
atg tgg aac ccg aac aca ccg ctc tcg gag gac tgt ctg tac atc aac	241
Met Trp Asn Pro Asn Thr 70 Pro Leu Ser Glu Asp 75 Cys Leu Tyr Ile Asn 80	
gtg gtc gtg cca cgg ccc agg ccc aag aat gcc gcc gtc atg ctg tgg	289
Val Val Val Pro 85 Arg Pro Arg Pro Lys Asn 90 Ala Ala Val Met Leu 95 Trp	
atc ttc ggg ggt ggc ttc tac tcc ggg act gcc acg ctg gac gtg tac	337
Ile Phe Gly Gly 100 Gly Phe Tyr Ser Gly 105 Thr Ala Thr Leu 110 Asp Val Tyr	
gac cac cgg acg ctg gcc tcg gag gag aac gtg atc gta gtt tcg ctg	385
Asp His Arg 115 Thr Leu Ala Ser Glu 120 Glu Asn Val Ile 125 Val Val Ser Leu	
cag tac cgt gtc gca agt ctt ggg ttt ct	414
Gln Tyr 130 Arg Val Ala Ser Leu 135 Gly Phe	

263365US0XPCT

<210> 83
 <211> 437
 <212> DNA
 <213> Culex pipiens quinquefasciatus strain Bouake (R)

<220>
 <221> CDS
 <222> (3)..(434)

<400> 83
 ag ggc aaa atc cgt gga acg aca ctg gaa gcg cct agt gga aag aag 47
 Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys
 1 5 10 15
 gtg gac gca tgg atg ggc att ccg tac gcg cag ccc ccg ctg ggt ccg 95
 Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro
 20 25 30
 ctc cgg ttt cga cat ccg cga ccc gcc gaa aga tgg acc ggt gtg ctg 143
 Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu
 35 40 45
 aac gcg acc aaa ccg ccc aac tcc tgc gtc cag atc gtg gac acc gtg 191
 Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val
 50 55 60
 ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg aac aca ccg ctc 239
 Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu
 65 70 75
 tcg gag gac tgt ctg tac atc aac gtg gtc gtg cca cgg ccc agg ccc 287
 Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro
 80 85 90 95
 aag aat gcc gcc gtc atg ctg tgg atc ttc ggg ggt ggc ttc tac tcc 335
 Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser
 100 105 110
 ggg act gcc acg ctg gac gtg tac gac cac cgg acg ctg gcc tcg gag 383
 Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu
 115 120 125
 gag aac gtg atc gta gtt tcg ctg cag tac cgt gtc gca agt ctt ggt 431
 Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly
 130 135 140
 ttt ctc 437
 Phe

<210> 84
 <211> 416
 <212> DNA
 <213> Culex pipiens quinquefasciatus strain Thai (S)

<220>
 <221> CDS
 <222> (1)..(414)

<400> 84
 aca ctg gaa gcg cct agt gga aag aag gtg gac gcc tgg atg ggc att 48
 Thr Leu Glu Ala Pro Ser Gly Lys Lys Val Asp Ala Trp Met Gly Ile
 1 5 10 15
 ccg tac gcg cag ccc ccg ctg ggt ccg ctc cgg ttt cga cat ccg cga 96
 Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu Arg Phe Arg His Pro Arg
 20 25 30

263365US0XPCT

ccc gcc gaa aga tgg acc ggt gtg ctg aac gcg acc aaa ccg ccc aac	144
Pro Ala Glu Arg Trp Thr Gly Val Leu Asn Ala Thr Lys Pro Pro Asn	
35 40 45	
tcc tgc gtc cag atc gtg gac acc gtg ttc ggt gac ttc ccg ggg gcc	192
Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala	
50 55 60	
acc atg tgg aac ccg aac aca ccg ctc tcg gag gac tgt ctg tac atc	240
Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile	
65 70 75 80	
aac gtg gtc gtg cca cgg ccc agg ccc aag aat gcc gcc gtc atg ctg	288
Asn Val Val Val Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu	
85 90 95	
tgg atc ttc ggg ggt ggc ttc tac tcc ggg act gcc acg ctg gac gtg	336
Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val	
100 105 110	
tac gac cac cgg acg ctg gcc tcg gag gag aac gtg atc gta gtt tcg	384
Tyr Asp His Arg Thr Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser	
115 120 125	
ctg cag tac cgt gtc gca agt ctt ggg ttt ct	416
Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe	
130 135	

<210> 85

<211> 426

<212> DNA

<213> Culex pipiens quinquefasciatus strain Madurai (S)

<220>

<221> CDS

<222> (3)..(425)

<400> 85

ca ctg gaa gcg cct agt gga aag aag gtg gac gca tgg atg ggc att	47
Leu Glu Ala Pro Ser Gly Lys Lys Val Asp Ala Trp Met Gly Ile	
1 5 10 15	
ccg tac gcg cag ccc ccg ctg ggt ccg ctc ccg ttt cga cat ccg cga	95
Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu Arg Phe Arg His Pro Arg	
20 25 30	
ccc gcc gaa aga tgg acc ggt gtg ctg aac gca acc aaa ccg ccc aac	143
Pro Ala Glu Arg Trp Thr Gly Val Leu Asn Ala Thr Lys Pro Pro Asn	
35 40 45	
tcc tgc gtc cag atc gtg gac acc gtg ttc ggt gac ttc ccg ggg gcc	191
Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala	
50 55 60	
acc atg tgg aac ccg aac aca ccg ctc tcg gag gac tgt ctg tac atc	239
Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile	
65 70 75	
aac gtg gtc gtg cca cgg ccc agg ccc aag aat gcc gcc gtc atg ctg	287
Asn Val Val Val Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu	
80 85 90 95	
tgg atc ttc ggg ggt ggc ttc tac tcc ggg act gcc acg ctg gac gtg	335
Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val	
100 105 110	
tac gac cac cgg acg ctg gcc tcg gag gag aac gtg atc gta gtt tcg	383

263365US0XPCT

Tyr Asp His Arg Thr Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser
115 120 125

ctg cag tac cgt gtc gca agt ctt ggg ttt ctc ttc ctg ggc a 426
Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu Phe Leu Gly
130 135 140

<210> 86
<211> 423
<212> DNA
<213> Culex pipiens quinquefasciatus strain Recife (R)

<220>
<221> CDS
<222> (1)..(423)

<400> 86
ctg gaa gcg cct agc gga aag aag gtg gac gca tgg atg ggc att ccg 48
Leu Glu Ala Pro Ser Gly Lys Lys Val Asp Ala Trp Met Gly Ile Pro
1 5 10 15

tac gcg cag cct ccg ctg ggt ccg ctc cgg ttt cga cat ccg cga ccc 96
Tyr Ala Gln Pro Pro Leu Gly Pro Leu Arg Phe Arg His Pro Arg Pro
20 25 30

gcc gaa aga tgg acc ggt gtg ctg aac gcg acc aaa ccg ccc aac tcc 144
Ala Glu Arg Trp Thr Gly Val Leu Asn Ala Thr Lys Pro Pro Asn Ser
35 40 45

tgc gtc cag atc gtg gac acc gtg ttc ggt gac ttc ccg ggg gcc acc 192
Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala Thr
50 55 60

atg tgg aac ccg aac aca ccg ctc tcg gag gac tgt ctg tac atc aac 240
Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile Asn
65 70 75 80

gtg gtc gtg cca cgg ccc agg ccc aag aat gcc gcc gtc atg ctg tgg 288
Val Val Val Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu Trp
85 90 95

atc ttc ggg ggt agc ttc tac tcc ggg act gcc acg ctg gac gtg tac 336
Ile Phe Gly Gly Ser Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val Tyr
100 105 110

gac cac cgg acg ctg gcc tcg gag gag aac gtg atc gta gtt tcg ctg 384
Asp His Arg Thr Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser Leu
115 120 125

cag tac cgt gtc gca agt ctt ggt ttt ctc ttc ctg ggc 423
Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu Phe Leu Gly
130 135 140

<210> 87
<211> 416
<212> DNA
<213> Culex pipiens quinquefasciatus strain Brasil (S)

<220>
<221> CDS
<222> (3)..(413)

<400> 87
ca ctg gaa gcg cct agt gga aag aag gtg gac gca tgg atg ggc att 47
Leu Glu Ala Pro Ser Gly Lys Lys Val Asp Ala Trp Met Gly Ile
1 5 10 15

263365US0XPCT

ccg	tac	gcg	cag	ccc	ccg	ctg	ggt	ccg	ctc	cg	ttt	cga	cat	ccg	cga	95
Pro	Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Pro	Leu	Arg	Phe	Arg	His	Pro	Arg	
				20					25					30		
ccc	gcc	gaa	aga	tgg	acc	ggt	gtg	ctg	aac	gcg	acc	aaa	ccg	ccc	aac	143
Pro	Ala	Glu	Arg	Trp	Thr	Gly	Val	Leu	Asn	Ala	Thr	Lys	Pro	Pro	Asn	
			35					40					45			
tcc	tgc	gtc	cag	atc	gtg	gac	acc	gtg	ttc	ggt	gac	ttc	ccg	ggg	gcc	191
Ser	Cys	Val	Gln	Ile	Val	Asp	Thr	Val	Phe	Gly	Asp	Phe	Pro	Gly	Ala	
		50					55					60				
acc	atg	tgg	aac	ccg	aac	aca	ccg	ctc	tcg	gag	gac	tgt	ctg	tac	atc	239
Thr	Met	Trp	Asn	Pro	Asn	Thr	Pro	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Ile	
	65					70					75					
aac	gtg	gtc	gtg	cca	cgg	ccc	agg	ccc	aag	aat	gcc	gcc	gtc	atg	ctg	287
Asn	Val	Val	Val	Pro	Arg	Pro	Arg	Pro	Lys	Asn	Ala	Ala	Val	Met	Leu	
80					85					90					95	
tgg	atc	ttc	ggg	ggt	ggc	ttc	tat	tcc	ggg	act	gcc	acg	ctg	gac	gtg	335
Trp	Ile	Phe	Gly	Gly	Gly	Phe	Tyr	Ser	Gly	Thr	Ala	Thr	Leu	Asp	Val	
				100					105					110		
tac	gac	cac	cgg	acg	ctg	gcc	tcg	gag	gag	aac	gtg	atc	gta	gtt	tcg	383
Tyr	Asp	His	Arg	Thr	Leu	Ala	Ser	Glu	Glu	Asn	Val	Ile	Val	Val	Ser	
			115					120					125			
ctg	cag	tac	cgt	gtc	gca	agt	ctt	ggg	ttt	ctc						416
Leu	Gln	Tyr	Arg	Val	Ala	Ser	Leu	Gly	Phe							
		130					135									

<210> 88

<211> 418

<212> DNA

<213> Culex pipiens quinquefasciatus strain Moorea (S)

<220>

<221> CDS

<222> (1)..(417)

<400> 88

aca	ctg	gaa	gcg	cct	agt	gga	aag	aag	gtg	gac	gca	tgg	atg	ggc	att	48
Thr	Leu	Glu	Ala	Pro	Ser	Gly	Lys	Lys	Val	Asp	Ala	Trp	Met	Gly	Ile	
1				5					10					15		
ccg	tac	gcg	cag	cct	ccg	ctg	ggt	ccg	ctc	cg	ttt	cga	cat	ccg	cga	96
Pro	Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Pro	Leu	Arg	Phe	Arg	His	Pro	Arg	
			20					25					30			
ccc	gcc	gaa	aga	tgg	acc	ggt	gtg	ctg	aac	gcg	acc	aaa	ccg	ccc	aac	144
Pro	Ala	Glu	Arg	Trp	Thr	Gly	Val	Leu	Asn	Ala	Thr	Lys	Pro	Pro	Asn	
			35					40					45			
tcc	tgc	gtc	cag	atc	gtg	gac	acc	gtg	ttc	ggt	gac	ttc	ccg	ggg	gcc	192
Ser	Cys	Val	Gln	Ile	Val	Asp	Thr	Val	Phe	Gly	Asp	Phe	Pro	Gly	Ala	
	50					55					60					
acc	atg	tgg	aac	ccg	aac	aca	ccg	ctc	tcg	gag	gac	tgt	ctg	tac	atc	240
Thr	Met	Trp	Asn	Pro	Asn	Thr	Pro	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Ile	
	65				70					75					80	
aac	gtg	gtc	gtg	cca	cgg	ccc	agg	ccc	aag	aat	gcc	gcc	gtc	atg	ctg	288
Asn	Val	Val	Val	Pro	Arg	Pro	Arg	Pro	Lys	Asn	Ala	Ala	Val	Met	Leu	
				85					90					95		
tgg	atc	ttc	ggg	ggt	ggc	ttc	tac	tcc	ggg	act	gcc	acg	ctg	gac	gtg	336
Trp	Ile	Phe	Gly	Gly	Gly	Phe	Tyr	Ser	Gly	Thr	Ala	Thr	Leu	Asp	Val	

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100	105	110	
tac gac cac cgg acg ctg gcc tcg gag gag aac gtg atc gta gtt tcg Tyr Asp His Arg Thr Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser			384
ctg cag tac cgt gtc gca agt ctt ggg ttt ctc t Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu			418
<210> 89			
<211> 402			
<212> DNA			
<213> Culex pipiens pipiens strain Killcare (S)			
<220>			
<221> CDS			
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<400> 89			
agt gga aag aag gtg gac gca tgg atg ggc att ccg tac gcg cag ccc Ser Gly Lys Lys Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro			48
ccg ctg ggt ccg ctc cgg ttt cga cat ccg cga ccc gcc gaa aga tgg Pro Leu Gly Pro Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp			96
acc ggt gtg ctg aac gcg acc aaa cca ccc aac tcc tgc gtc cag atc Thr Gly Val Leu Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile			144
gtg gac aca gtg ttc ggt gac ttc ccg ggg gcc acc atg tgg aac ccg Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro			192
aac aca ccc ctc tcg gag gac tgt ctg tac atc aac gtg gtc gtg cca Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro			240
agg ccg agg ccc aag aat gcc gct gtc atg ctg tgg atc ttc ggg ggt Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly			288
ggc ttc tac tcc ggg act gcc acg ttg gac gtg tac gat cat cgg acg Gly Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr			336
ctg gcc tcg gag gag aac gtg atc gtg gtt tcg ctg cag tac cgt gtc Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val			384
gca agt ctt ggt ttt ctc Ala Ser Leu Gly Phe Leu			402
<210> 90			
<211> 152			
<212> PRT			
<213> Culex pipiens pipiens strain Espro (R)			
<400> 90			
Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val 1 5 10 15			
Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu 20 25 30			

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Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
35 40 45
Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
50 55 60
Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
65 70 75 80
Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
85 90 95
Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr Ser Gly
100 105 110
Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu
115 120 125
Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
130 135 140
Leu Phe Leu Gly Thr Pro Glu Ala
145 150

<210> 91
<211> 152
<212> PRT
<213> Culex pipiens quinquefasciatus strain ProR(S)

<400> 91
Lys Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys
1 5 10 15
Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro
20 25 30
Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu
35 40 45
Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val
50 55 60
Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu
65 70 75 80
Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro
85 90 95
Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser
100 105 110
Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu
115 120 125
Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly
130 135 140
Phe Leu Phe Leu Gly Thr Pro Glu
145 150

<210> 92
<211> 148
<212> PRT
<213> Culex pipiens pipiens strain S-LAB (S)

<400> 92

263365US0XPCT

Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val
 1 5 10 15
 Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu
 20 25 30
 Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
 35 40 45
 Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
 50 55 60
 Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
 65 70 75 80
 Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
 85 90 95
 Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly
 100 105 110
 Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu
 115 120 125
 Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
 130 135 140
 Leu Phe Leu Gly
 145

<210> 93

<211> 152

<212> PRT

<213> Culex pipiens pipiens strain Padova (R)

<400> 93

Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val
 1 5 10 15
 Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu
 20 25 30
 Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
 35 40 45
 Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
 50 55 60
 Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
 65 70 75 80
 Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
 85 90 95
 Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr Ser Gly
 100 105 110
 Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu
 115 120 125
 Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
 130 135 140
 Leu Phe Leu Gly Thr Pro Glu Ala
 145 150

<210> 94

<211> 154

263365US0XPCT

<212> PRT

<213> Culex pipiens pipiens strain Praias (R)

<400> 94

Asp Lys Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys
 1 5 10 15
 Lys Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly
 20 25 30
 Pro Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val
 35 40 45
 Leu Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr
 50 55 60
 Val Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro
 65 70 75 80
 Leu Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg
 85 90 95
 Pro Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr
 100 105 110
 Ser Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser
 115 120 125
 Glu Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu
 130 135 140
 Gly Phe Leu Phe Leu Gly Thr Pro Glu Ala
 145 150

<210> 95

<211> 154

<212> PRT

<213> Culex pipiens quinquefasciatus strain Supercar (R)

<400> 95

Asp Lys Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys
 1 5 10 15
 Lys Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly
 20 25 30
 Pro Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val
 35 40 45
 Leu Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr
 50 55 60
 Val Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro
 65 70 75 80
 Leu Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg
 85 90 95
 Pro Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr
 100 105 110
 Ser Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser
 115 120 125
 Glu Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu
 130 135 140
 Gly Phe Leu Phe Leu Gly Thr Pro Glu Ala

145

150

<210> 96

<211> 148

<212> PRT

<213> Culex pipiens pipiens strain Bruges A (S)

<400> 96

Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val
 1 5 10 15
 Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu
 20 25 30
 Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
 35 40 45
 Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
 50 55 60
 Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
 65 70 75 80
 Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
 85 90 95
 Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly
 100 105 110
 Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu
 115 120 125
 Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
 130 135 140
 Leu Phe Leu Gly
 145

<210> 97

<211> 152

<212> PRT

<213> Culex pipiens quinquefasciatus strain BO (R)

<400> 97

Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val
 1 5 10 15
 Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu
 20 25 30
 Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
 35 40 45
 Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
 50 55 60
 Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
 65 70 75 80
 Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
 85 90 95
 Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr Ser Gly
 100 105 110
 Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu
 115 120 125
 Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
 130 135 140
 Leu Phe Leu Gly
 145

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115 120 125
 Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
 130 135 140
 Leu Phe Leu Gly Thr Pro Glu Ala
 145 150
 <210> 98
 <211> 148
 <212> PRT
 <213> Culex pipiens quinquefasciatus strain DJI (R)
 <400> 98
 Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val
 1 5 10 15
 Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu
 20 25 30
 Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
 35 40 45
 Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
 50 55 60
 Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
 65 70 75 80
 Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
 85 90 95
 Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr Ser Gly
 100 105 110
 Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu
 115 120 125
 Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
 130 135 140
 Leu Phe Leu Gly
 145

<210> 99
 <211> 152
 <212> PRT
 <213> Culex pipiens quinquefasciatus strain Harare (R)

<400> 99
 Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val
 1 5 10 15
 Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu
 20 25 30
 Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
 35 40 45
 Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
 50 55 60
 Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
 65 70 75 80
 Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
 85 90 95

Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr Ser Gly
 100 105 110
 Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu
 115 120 125
 Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
 130 135 140
 Leu Phe Leu Gly Thr Pro Glu Ala
 145 150

<210> 100

<211> 152

<212> PRT

<213> Culex pipiens quinquefasciatus strain Martinique (R)

<400> 100

Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val
 1 5 10 15
 Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu
 20 25 30
 Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
 35 40 45
 Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
 50 55 60
 Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
 65 70 75 80
 Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
 85 90 95
 Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Ser Phe Tyr Ser Gly
 100 105 110
 Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu
 115 120 125
 Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
 130 135 140
 Leu Phe Leu Gly Thr Pro Glu Ala
 145 150

<210> 101

<211> 148

<212> PRT

<213> Culex pipiens pipiens strain Barriol (R)

<400> 101

Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val
 1 5 10 15
 Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu
 20 25 30
 Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
 35 40 45
 Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
 50 55 60
 Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
 65 70 75 80

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<210> 102
<211> 148
<212> PRT
<213> Culex pipiens pipiens strain Bleuet (S)

[illegible]

<210> 103
<211> 148
<212> PRT
<213> Culex pipiens pipiens strain Bruges B (S)

<400> 103
Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val
1 5 10 15
Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu
20 25 30
Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
35 40 45
Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
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60

50

55

60

Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
65 70 75 80
Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
85 90 95
Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly
100 105 110
Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu
115 120 125
Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
130 135 140
Leu Phe Leu Gly
145

<210> 104

<211> 148

<212> PRT

<213> Culex pipiens pipiens strain Heteren (S)

<400> 104

Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val
1 5 10 15
Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu
20 25 30
Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
35 40 45
Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
50 55 60
Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
65 70 75 80
Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
85 90 95
Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly
100 105 110
Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu
115 120 125
Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
130 135 140
Leu Phe Leu Gly
145

<210> 105

<211> 149

<212> PRT

<213> Culex pipiens quinquefasciatus strain Ling (S)

<400> 105

Gln Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys
1 5 10 15
Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro
20 25 30

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Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu
 35 40 45
 Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val
 50 55 60
 Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu
 65 70 75 80
 Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro
 85 90 95
 Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser
 100 105 110
 Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu
 115 120 125
 Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly
 130 135 140
 Phe Leu Phe Leu Gly
 145

<210> 106
 <211> 148
 <212> PRT
 <213> Culex pipiens quinquefasciatus strain Mao (S)

<400> 106
 Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val
 1 5 10 15
 Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu
 20 25 30
 Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
 35 40 45
 Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
 50 55 60
 Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
 65 70 75 80
 Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
 85 90 95
 Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly
 100 105 110
 Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu
 115 120 125
 Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
 130 135 140
 Leu Phe Leu Gly
 145

<210> 107
 <211> 144
 <212> PRT
 <213> Culex pipiens quinquefasciatus strain TemR (S)

<400> 107
 Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val Asp
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1 5 10 15
 Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu Arg
 20 25 30
 Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn Ala
 35 40 45
 Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly
 50 55 60
 Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu
 65 70 75 80
 Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys Asn
 85 90 95
 Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr
 100 105 110
 Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Thr Ser Glu Glu Asn
 115 120 125
 Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu
 130 135 140

<210> 108

<211> 148

<212> PRT

<213> Culex torrentium strain Uppsala

<400> 108

Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val
 1 5 10 15
 Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu
 20 25 30
 Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
 35 40 45
 Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
 50 55 60
 Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
 65 70 75 80
 Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
 85 90 95
 Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly
 100 105 110
 Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Ala Ser Glu Glu
 115 120 125
 Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
 130 135 140

Leu Phe Leu Gly
 145

<210> 109

<211> 148

<212> PRT

<213> Culex pipiens quinquefasciatus strain Trans (S)

<400> 109

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Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val
 1 5 10 15
 Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu
 20 25 30
 Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp Thr Gly Val Leu Asn
 35 40 45
 Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe
 50 55 60
 Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser
 65 70 75 80
 Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro Arg Pro Arg Pro Lys
 85 90 95
 Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly
 100 105 110
 Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr Leu Thr Ser Glu Glu
 115 120 125
 Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe
 130 135 140
 Leu Phe Leu Gly
 145

<210> 110

<211> 137

<212> PRT

<213> Culex pipiens quinquefasciatus strain BED (S)

<400> 110

Thr Leu Glu Ala Pro Ser Gly Lys Lys Val Asp Ala Trp Met Gly Ile
 1 5 10 15
 Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu Arg Phe Arg His Pro Arg
 20 25 30
 Pro Ala Glu Arg Trp Thr Gly Val Leu Asn Ala Thr Lys Pro Pro Asn
 35 40 45
 Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala
 50 55 60
 Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile
 65 70 75 80
 Asn Val Val Val Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu
 85 90 95
 Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val
 100 105 110
 Tyr Asp His Arg Thr Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser
 115 120 125
 Leu Gln Tyr Arg Val Ala Ser Leu Gly
 130 135

<210> 111

<211> 144

<212> PRT

<213> Culex pipiens quinquefasciatus strain BSQ (S)

263365US0XPCT

<400> 111

Gly₁ Lys Ile Arg Gly₅ Thr Thr Leu Glu Ala₁₀ Pro Ser Gly Lys Lys Val
 Asp Ala Trp Met₂₀ Gly Ile Pro Tyr Ala₂₅ Gln Pro Pro Leu Gly₃₀ Pro Leu
 Arg Phe Arg₃₅ His Pro Arg Pro Ala₄₀ Glu Arg Trp Thr Gly₄₅ Val Leu Asn
 Ala Thr Lys₅₀ Pro Pro Asn Ser₅₅ Cys Val Gln Ile Val₆₀ Asp Thr Val Phe
 Gly₆₅ Asp Phe Pro Gly Ala₇₀ Thr Met Trp Asn₇₅ Asn Thr Pro Leu Ser₈₀
 Glu Asp Cys Leu Tyr₈₅ Ile Asn Val Val₉₀ Val Pro Arg Pro Arg₉₅ Pro Lys
 Asn Ala Ala Val₁₀₀ Met Leu Trp Ile Phe₁₀₅ Gly Gly Gly Phe Tyr₁₁₀ Ser Gly
 Thr Ala Thr₁₁₅ Leu Asp Val Tyr Asp₁₂₀ His Arg Thr Leu Ala₁₂₅ Ser Glu Glu
 Asn Val₁₃₀ Ile Val Val Ser₁₃₅ Leu Gln Tyr Arg Val₁₄₀ Ala Ser Leu Gly Phe

<210> 112

<211> 137

<212> PRT

<213> Culex pipiens quinquefasciatus strain Brazza (S)

<400> 112

Leu₁ Glu Ala Pro Ser₅ Gly Lys Lys Val₁₀ Asp Ala Trp Met Gly Ile₁₅ Pro
 Tyr Ala Gln₂₀ Pro Pro Leu Gly Pro Leu₂₅ Arg Phe Arg His Pro₃₀ Arg Pro
 Ala Glu Arg₃₅ Trp Thr Gly Val₄₀ Asn Ala Thr Lys₄₅ Pro Pro Asn Ser
 Cys Val₅₀ Gln Ile Val Asp₅₅ Thr Val Phe Gly Asp Phe₆₀ Pro Gly Ala Thr
 Met₆₅ Trp Asn Pro Asn₇₀ Thr Pro Leu Ser Glu Asp₇₅ Cys Leu Tyr Ile Asn₈₀
 Val Val Val₈₅ Pro Arg Pro Arg Pro Lys₉₀ Asn Ala Ala Val₉₅ Met Leu Trp
 Ile Phe Gly₁₀₀ Gly Phe Tyr Ser Gly₁₀₅ Thr Ala Thr Leu Asp₁₁₀ Val Tyr
 Asp His Arg₁₁₅ Thr Leu Ala Ser Glu₁₂₀ Glu Asn Val Ile Val₁₂₅ Val Ser Leu
 Gln Tyr Arg Val₁₃₀ Ala Ser Leu₁₃₅ Gly Phe

<210> 113

<211> 144

<212> PRT

<213> Culex pipiens quinquefasciatus strain Bouake (R)

<400> 113

Gly Lys Ile Arg Gly Thr Thr Leu Glu Ala Pro Ser Gly Lys Lys Val
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1	5	10	15												
Asp	Ala	Trp	Met	Gly	Ile	Pro	Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Pro	Leu
			20					25					30		
Arg	Phe	Arg	His	Pro	Arg	Pro	Ala	Glu	Arg	Trp	Thr	Gly	Val	Leu	Asn
		35					40					45			
Ala	Thr	Lys	Pro	Pro	Asn	Ser	Cys	Val	Gln	Ile	Val	Asp	Thr	Val	Phe
		50				55					60				
Gly	Asp	Phe	Pro	Gly	Ala	Thr	Met	Trp	Asn	Pro	Asn	Thr	Pro	Leu	Ser
65					70					75					80
Glu	Asp	Cys	Leu	Tyr	Ile	Asn	Val	Val	Val	Pro	Arg	Pro	Arg	Pro	Lys
				85					90					95	
Asn	Ala	Ala	Val	Met	Leu	Trp	Ile	Phe	Gly	Gly	Gly	Phe	Tyr	Ser	Gly
			100					105					110		
Thr	Ala	Thr	Leu	Asp	Val	Tyr	Asp	His	Arg	Thr	Leu	Ala	Ser	Glu	Glu
		115					120					125			
Asn	Val	Ile	Val	Val	Ser	Leu	Gln	Tyr	Arg	Val	Ala	Ser	Leu	Gly	Phe
		130				135					140				

<210> 114

<211> 138

<212> PRT

<213> Culex pipiens quinquefasciatus strain Thai (S)

<400> 114

Thr	Leu	Glu	Ala	Pro	Ser	Gly	Lys	Lys	Val	Asp	Ala	Trp	Met	Gly	Ile
1				5					10					15	
Pro	Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Pro	Leu	Arg	Phe	Arg	His	Pro	Arg
			20					25					30		
Pro	Ala	Glu	Arg	Trp	Thr	Gly	Val	Leu	Asn	Ala	Thr	Lys	Pro	Pro	Asn
		35					40					45			
Ser	Cys	Val	Gln	Ile	Val	Asp	Thr	Val	Phe	Gly	Asp	Phe	Pro	Gly	Ala
	50					55					60				
Thr	Met	Trp	Asn	Pro	Asn	Thr	Pro	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Ile
65					70					75					80
Asn	Val	Val	Val	Pro	Arg	Pro	Arg	Pro	Lys	Asn	Ala	Ala	Val	Met	Leu
				85					90					95	
Trp	Ile	Phe	Gly	Gly	Gly	Phe	Tyr	Ser	Gly	Thr	Ala	Thr	Leu	Asp	Val
			100					105					110		
Tyr	Asp	His	Arg	Thr	Leu	Ala	Ser	Glu	Glu	Asn	Val	Ile	Val	Val	Ser
		115					120					125			
Leu	Gln	Tyr	Arg	Val	Ala	Ser	Leu	Gly	Phe						
		130				135									

<210> 115

<211> 141

<212> PRT

<213> Culex pipiens quinquefasciatus strain Madurai (S)

<400> 115

Leu	Glu	Ala	Pro	Ser	Gly	Lys	Lys	Val	Asp	Ala	Trp	Met	Gly	Ile	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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1				5				10				15			
Tyr	Ala	Gln	Pro ₂₀	Pro	Leu	Gly	Pro	Leu ₂₅	Arg	Phe	Arg	His	Pro ₃₀	Arg	Pro
Ala	Glu	Arg ₃₅	Trp	Thr	Gly	Val	Leu ₄₀	Asn	Ala	Thr	Lys	Pro ₄₅	Pro	Asn	Ser
Cys	Val ₅₀	Gln	Ile	Val	Asp	Thr ₅₅	Val	Phe	Gly	Asp	Phe ₆₀	Pro	Gly	Ala	Thr
Met ₆₅	Trp	Asn	Pro	Asn	Thr ₇₀	Pro	Leu	Ser	Glu	Asp ₇₅	Cys	Leu	Tyr	Ile	Asn ₈₀
Val	Val	Val	Pro	Arg ₈₅	Pro	Arg	Pro	Lys	Asn ₉₀	Ala	Ala	Val	Met	Leu ₉₅	Trp
Ile	Phe	Gly	Gly ₁₀₀	Gly	Phe	Tyr	Ser	Gly ₁₀₅	Thr	Ala	Thr	Leu	Asp ₁₁₀	Val	Tyr
Asp	His	Arg ₁₁₅	Thr	Leu	Ala	Ser	Glu ₁₂₀	Glu	Asn	Val	Ile	Val ₁₂₅	Val	Ser	Leu
Gln	Tyr ₁₃₀	Arg	Val	Ala	Ser	Leu ₁₃₅	Gly	Phe	Leu	Phe	Leu ₁₄₀	Gly			

<210> 116

<211> 141

<212> PRT

<213> *Culex pipiens quinquefasciatus* strain Recife (R)

<400> 116

Leu ₁	Glu	Ala	Pro	Ser ₅	Gly	Lys	Lys	Val	Asp ₁₀	Ala	Trp	Met	Gly	Ile ₁₅	Pro
Tyr	Ala	Gln	Pro ₂₀	Pro	Leu	Gly	Pro	Leu ₂₅	Arg	Phe	Arg	His	Pro ₃₀	Arg	Pro
Ala	Glu	Arg ₃₅	Trp	Thr	Gly	Val	Leu ₄₀	Asn	Ala	Thr	Lys	Pro ₄₅	Pro	Asn	Ser
Cys	Val ₅₀	Gln	Ile	Val	Asp	Thr ₅₅	Val	Phe	Gly	Asp	Phe ₆₀	Pro	Gly	Ala	Thr
Met ₆₅	Trp	Asn	Pro	Asn	Thr ₇₀	Pro	Leu	Ser	Glu	Asp ₇₅	Cys	Leu	Tyr	Ile	Asn ₈₀
Val	Val	Val	Pro	Arg ₈₅	Pro	Arg	Pro	Lys	Asn ₉₀	Ala	Ala	Val	Met	Leu ₉₅	Trp
Ile	Phe	Gly	Gly ₁₀₀	Ser	Phe	Tyr	Ser	Gly ₁₀₅	Thr	Ala	Thr	Leu	Asp ₁₁₀	Val	Tyr
Asp	His	Arg ₁₁₅	Thr	Leu	Ala	Ser	Glu ₁₂₀	Glu	Asn	Val	Ile	Val ₁₂₅	Val	Ser	Leu
Gln	Tyr ₁₃₀	Arg	Val	Ala	Ser	Leu ₁₃₅	Gly	Phe	Leu	Phe	Leu ₁₄₀	Gly			

<210> 117

<211> 137

<212> PRT

<213> *Culex pipiens quinquefasciatus* strain Brasil (S)

<400> 117

Leu Glu Ala Pro Ser Gly Lys Lys Val Asp Ala Trp Met Gly Ile Pro
1 5 10 15

263365US0XPCT

Tyr Ala Gln Pro Pro Leu Gly Pro Leu Arg Phe Arg His Pro Arg Pro
20 25 30
Ala Glu Arg Trp Thr Gly Val Leu Asn Ala Thr Lys Pro Pro Asn Ser
35 40 45
Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala Thr
50 55 60
Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile Asn
65 70 75 80
Val Val Val Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu Trp
85 90 95
Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val Tyr
100 105 110
Asp His Arg Thr Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser Leu
115 120 125
Gln Tyr Arg Val Ala Ser Leu Gly Phe
130 135

<210> 118

<211> 139

<212> PRT

<213> Culex pipiens quinquefasciatus strain Moorea (S)

<400> 118

Thr Leu Glu Ala Pro Ser Gly Lys Lys Val Asp Ala Trp Met Gly Ile
1 5 10 15
Pro Tyr Ala Gln Pro Pro Leu Gly Pro Leu Arg Phe Arg His Pro Arg
20 25 30
Pro Ala Glu Arg Trp Thr Gly Val Leu Asn Ala Thr Lys Pro Pro Asn
35 40 45
Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala
50 55 60
Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile
65 70 75 80
Asn Val Val Val Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu
85 90 95
Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val
100 105 110
Tyr Asp His Arg Thr Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser
115 120 125
Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu
130 135

<210> 119

<211> 134

<212> PRT

<213> Culex pipiens pipiens strain Killcare (S)

<400> 119

Ser Gly Lys Lys Val Asp Ala Trp Met Gly Ile Pro Tyr Ala Gln Pro
1 5 10 15

263365US0XPCT

Pro Leu Gly Pro Leu Arg Phe Arg His Pro Arg Pro Ala Glu Arg Trp
 20 25 30
 Thr Gly Val Leu Asn Ala Thr Lys Pro Pro Asn Ser Cys Val Gln Ile
 35 40 45
 Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala Thr Met Trp Asn Pro
 50 55 60
 Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile Asn Val Val Val Pro
 65 70 75 80
 Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu Trp Ile Phe Gly Gly
 85 90 95
 Gly Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val Tyr Asp His Arg Thr
 100 105 110
 Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser Leu Gln Tyr Arg Val
 115 120 125
 Ala Ser Leu Gly Phe Leu
 130

<210> 120

<211> 2527

<212> DNA

<213> Anopheles gambiae strain YAO

<400> 120

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tgacatgttt	gtgtgttgtt	ttttctttct	cttctctctt	ctttctgttg	ttccaacatt	120
tcagacgcat	tttttacacc	atatatatgg	cacggtgagt	ccgcacgaat	tatagatgcc	180
gagttgggca	cgctcgagca	tgtacacagt	ggagcaacgc	cgcggcgacg	cggtctgacg	240
aggcgcgagt	caaactcggg	taagtacgcg	attggaagtg	gggggacgtt	taccctaccg	300
tgtactacaa	cgcactttac	ccccacgcac	acgcaccggc	agacgcgaac	gacaacgatc	360
cgctgggtgt	caacacggat	aaggggcgca	tccgcggcat	tacggtcgat	gccccagcg	420
gcaagaagggt	ggacgtgtgg	ctcggcattc	cctacgcccc	gccgcccgtc	gggcccgtac	480
ggttccgtca	tccgcggccc	gccgaaaagt	ggaccggcgt	gctgaacacg	accacaccgc	540
ccaacagctg	cgtgcagatc	gtggacaccg	tgttcggcga	cttcccgggc	gcgaccatgt	600
ggaacccgaa	cacgccccct	tccgaggact	gtctgtacat	taacgtgggt	gcaccgcggc	660
cccggcccaa	gaatgcggcc	gtcatgttgt	ggatcttcgg	cggcagcttc	tactccggca	720
ccgccaccct	ggacgtgtac	gaccaccggg	cgcttgcgct	ggaggagaac	gtgatcgtgg	780
tgctcgctga	gtaccgcgtg	gccagtcctg	gcttctctgt	tctcggcacc	ccggaagcgc	840
cgggcaatgc	gggactgttc	gatcagaaac	ttgcgctacg	gtaggtgtct	ttgcgtgtgt	900
gtctgtagtt	atagatttct	aacgaggtgc	tcttcttccc	atcacttctt	gggagtcagc	960
tgggtgcggg	acaacattca	ccggttcggc	ggatgatccgt	cgcgctgac	actgttcggc	1020
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gaggaagcca	cgctaaggta	cgtgccagct	gctgctttcc	ccaaaccacc	aaccgcgaac	1200
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acccgtggcc	gcgctggacg	ggcgtgatgc	acggcgacga	gatcaactac	gtgttcggcg	1860
aaccgctcaa	ccccaccctc	ggctacaccg	aggacgagaa	agacttttagc	cggaagatca	1920
tgcgatactg	gtctaacttt	gccaaaaccg	ggtaagtgtg	tgtgtcaaac	agcaaagtgc	1980
caatagctct	aacaccagcg	tcttctctct	tctacagcaa	tccaaatccc	aacacagcca	2040
gcagcgaatt	ccccgagtgg	cccaagcaca	ccgcccacgg	acggcactat	ctggagctgg	2100
gcctcaacac	gtccttcgtc	ggtcggggcc	cacggttgag	gcagtgtgcc	ttctggaaga	2160
agtaccttcc	ccagctagtt	gcagctacct	gtaagtctag	ttgctgcacg	agaaaccccc	2220

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cgcatttttt taccgacctg atctgatcgt gctgctgggt tgcgtgctta cggcgaccgt 2400
cagattcata caataattac taccatcatcc atggccctagt tcgtttaagc ttttaagatag 2460
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<210> 121

<211> 2214

<212> DNA

<213> Anopheles gambiae strain YAO

<220>

<221> CDS

<222> (1)..(2214)

<400> 121

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Met Glu Ile Arg Gly Leu Leu Met Gly Arg Leu Arg Leu Gly Arg Arg
1 5 10 15

atg gtt ccg ctg ggt ctg ctc ggc gtg acc gcg ctg cta cta atc ctg 96
Met Val Pro Leu Gly Leu Leu Gly Val Thr Ala Leu Leu Leu Ile Leu
20 25 30

cca ccc tcc gcg ctg gtg cag ggc cgg cac cac gag ctc aac aat ggt 144
Pro Pro Ser Ala Leu Val Gln Gly Arg His His Glu Leu Asn Asn Gly
35 40 45

gcc gcc atc gga tcg cat cag ctg tcg gct gcc gcc ggt gtt ggc ctt 192
Ala Ala Ile Gly Ser His Gln Leu Ser Ala Ala Ala Gly Val Gly Leu
50 55 60

tcc tcc cag tcc gcc cag tcc gga tcg ctc gca tcc ggt gtg atg tca 240
Ser Ser Gln Ser Ala Gln Ser Gly Ser Leu Ala Ser Gly Val Met Ser
65 70 75 80

tcc gtt cct gct gcc gga gcg tca tcc tcc tcc tcg tcg tcg ctg ctg 288
Ser Val Pro Ala Ala Gly Ala Ser Ser Ser Ser Ser Ser Leu Leu
85 90 95

tca tcg tca gcc gag gac gac gtg gcg cgc att act ctc agc aag gac 336
Ser Ser Ser Ala Glu Asp Asp Val Ala Arg Ile Thr Leu Ser Lys Asp
100 105 110

gca gac gca ttt ttt aca cca tat ata ggt cac ggt gag tcc gca cga 384
Ala Asp Ala Phe Phe Thr Pro Tyr Ile Gly His Gly Glu Ser Ala Arg
115 120 125

att ata gat gcc gag ttg ggc acg ctc gag cat gta cac agt gga gca 432
Ile Ile Asp Ala Glu Leu Gly Thr Leu Glu His Val His Ser Gly Ala
130 135 140

acg ccg cgg cga cgc ggt ctg acg agg cgc gag tca aac tcg gac gcg 480
Thr Pro Arg Arg Arg Gly Leu Thr Arg Arg Glu Ser Asn Ser Asp Ala
145 150 155 160

aac gac aac gat ccg ctg gtg gtc aac acg gat aag ggg cgc atc cgc 528
Asn Asp Asn Asp Pro Leu Val Val Asn Thr Asp Lys Gly Arg Ile Arg
165 170 175

ggc att acg gtc gat gcc ccc agc ggc aag aag gtg gac gtg tgg ctc 576
Gly Ile Thr Val Asp Ala Pro Ser Gly Lys Lys Val Asp Val Trp Leu
180 185 190

ggc att ccc tac gcc cag ccg ccg gtc ggc ccg cta cgg ttc cgt cat 624
Gly Ile Pro Tyr Ala Gln Pro Pro Val Gly Pro Leu Arg Phe Arg His

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263365US0XPCT

195					200					205						
ccg Pro	cgg Arg 210	ccg Pro	gcc Ala	gaa Glu	aag Lys	tgg Trp 215	acc Thr	ggc Gly	gtg Val	ctg Leu	aac Asn 220	acg Thr	acc Thr	aca Thr	ccg Pro	672
ccc Pro 225	aac Asn	agc Ser	tgc Cys	gtg Val	cag Gln 230	atc Ile	gtg Val	gac Asp	acc Thr	gtg Val 235	ttc Phe	ggc Gly	gac Asp	ttc Phe	ccg Pro 240	720
ggc Gly	gcg Ala	acc Thr	atg Met	tgg Trp 245	aac Asn	ccg Pro	aac Asn	acg Thr	ccc Pro 250	ctg Leu	tcc Ser	gag Glu	gac Asp	tgt Cys 255	ctg Leu	768
tac Tyr	att Ile	aac Asn	gtg Val 260	gtg Val	gca Ala	ccg Pro	cgg Arg	ccc Pro 265	cgg Arg	ccc Pro	aag Lys	aat Asn	gcg Ala 270	gcc Ala	gtc Val	816
atg Met	ctg Leu	tgg Trp 275	atc Ile	ttc Phe	ggc Gly	ggc Gly	agc Ser 280	ttc Phe	tac Tyr	tcc Ser	ggc Gly	acc Thr 285	gcc Ala	acc Thr	ctg Leu	864
gac Asp	gtg Val 290	tac Tyr	gac Asp	cac His	cgg Arg	gcg Ala 295	ctt Leu	gcg Ala	tcg Ser	gag Glu	gag Glu 300	aac Asn	gtg Val	atc Ile	gtg Val	912
gtg Val 305	tcg Ser	ctg Leu	cag Gln	tac Tyr	cgc Arg 310	gtg Val	gcc Ala	agt Ser	ctg Leu	ggc Gly 315	ttc Phe	ctg Leu	ttt Phe	ctc Leu	ggc Gly 320	960
acc Thr	ccg Pro	gaa Glu	gcg Ala	ccg Pro 325	ggc Gly	aat Asn	gcg Ala	gga Gly	ctg Leu 330	ttc Phe	gat Asp	cag Gln	aac Asn	ctt Leu 335	gcg Ala	1008
cta Leu	cgc Arg	tgg Trp	gtg Val 340	cgg Arg	gac Asp	aac Asn	att Ile	cac His 345	cgg Arg	ttc Phe	ggt Gly	ggt Gly	gat Asp 350	ccg Pro	tcg Ser	1056
cgc Arg	gtg Val 355	aca Thr 355	ctg Leu	ttc Phe	ggc Gly	gag Glu	agt Ser 360	gcc Ala	ggt Gly	gcc Ala	gtc Val 365	tcg Ser 365	gtg Val	tcg Ser	ctg Leu	1104
cat His 370	ctg Leu	ctg Leu	tcc Ser	gcc Ala	ctt Leu	tcc Ser 375	cgc Arg	gat Asp	ctg Leu	ttc Phe	cag Gln 380	cgg Arg	gcc Ala	atc Ile	ctg Leu	1152
cag Gln 385	agc Ser	ggc Gly	tcg Ser	ccg Pro	acg Thr 390	gca Ala	ccg Pro	tgg Trp	gca Ala	ttg Leu 395	gta Val	tcg Ser	cgc Arg	gag Glu	gaa Glu 400	1200
gcc Ala	acg Thr	cta Leu	aga Arg	gca Ala 405	ctg Leu	cgg Arg	ttg Leu	gcc Ala	gag Glu 410	gcg Ala	gtc Val	ggc Gly	tgc Cys	ccg Pro 415	cac His	1248
gaa Glu	ccg Pro	agc Ser	aag Lys 420	ctg Leu	agc Ser	gat Asp	gcg Ala	gtc Val 425	gag Glu	tgt Cys	ctg Leu	cgc Arg	ggc Gly 430	aag Lys	gat Asp	1296
ccg Pro	cac His	gtg Val 435	ctg Leu	gtc Val	aac Asn	aac Asn	gag Glu 440	tgg Trp	ggc Gly	acg Thr	ctc Leu	ggc Gly 445	att Ile	tgc Cys	gag Glu	1344
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cag Gln	cgt Arg	tcg Ser	ctc Leu	gcc Ala	agc Ser	ggg Gly	cgc Arg	ttc Phe	aag Lys	aag Lys	acg Thr	gag Glu	atc Ile	ctc Leu	acc Thr	1440

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465											470	475					480	
ggc Gly	agc Ser	aac Asn	acg Thr	gag Glu 485	gag Glu	ggc Gly	tac Tyr	tac Tyr	ttc Phe 490	atc Ile	atc Ile	tac Tyr	tac Tyr	ctg Leu 495	acc Thr	1488		
gag Glu	ctg Leu	ctg Leu	cgc Arg 500	aag Lys	gag Glu	gag Glu	ggc Gly	gtg Val 505	acc Thr	gtg Val	acg Thr	cgc Arg	gag Glu 510	gag Glu	ttc Phe	1536		
ctg Leu	cag Gln	gcg Ala 515	gtg Val	cgc Arg	gag Glu	ctc Leu	aac Asn 520	ccg Pro	tac Tyr	gtg Val	aac Asn	ggg Gly 525	gcg Ala	gcc Ala	cgg Arg	1584		
cag Gln	gcg Ala 530	atc Ile	gtg Val	ttc Phe	gag Glu	tac Tyr 535	acc Thr	gac Asp	tgg Trp	acc Thr	gag Glu 540	ccg Pro	gac Asp	aac Asn	ccg Pro	1632		
aac Asn 545	agc Ser	aac Asn	cgg Arg	gac Asp	gcg Ala 550	ctg Leu	gac Asp	aag Lys	atg Met	gtg Val 555	ggc Gly	gac Asp	tat Tyr	cac His	ttc Phe 560	1680		
acc Thr	tgc Cys	aac Asn	gtg Val	aac Asn 565	gag Glu	ttc Phe	gcg Ala	cag Gln	cgg Arg 570	tac Tyr	gcc Ala	gag Glu	gag Glu	ggc Gly 575	aac Asn	1728		
aac Asn	gtc Val	tac Tyr	atg Met 580	tat Tyr	ctg Leu	tac Tyr	acg Thr	cac His 585	cgc Arg	agc Ser	aaa Lys	ggc Gly	aac Asn 590	ccg Pro	tgg Trp	1776		
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ggc Gly	gaa Glu 610	ccg Pro	ctc Leu	aac Asn	ccc Pro	acc Thr 615	ctc Leu	ggc Gly	tac Tyr	acc Thr	gag Glu 620	gac Asp	gag Glu	aaa Lys	gac Asp	1872		
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aat Asn	cca Pro	aat Asn	ccc Pro	aac Asn 645	aca Thr	gcc Ala	agc Ser	agc Ser	gaa Glu 650	ttc Phe	ccc Pro	gag Glu	tgg Trp	ccc Pro 655	aag Lys	1968		
cac His	acc Thr	gcc Ala	cac His 660	gga Gly	cgg Arg	cac His	tat Tyr	ctg Leu 665	gag Glu	ctg Leu	ggc Gly	ctc Leu	aac Asn 670	acg Thr	tcc Ser	2016		
ttc Phe	gtc Val	ggt Gly 675	cgg Arg	ggc Gly	cca Pro	cgg Arg	ttg Leu 680	agg Arg	cag Gln	tgt Cys	gcc Ala	ttc Phe 685	tgg Trp	aag Lys	aag Lys	2064		
tac Tyr	ctt Leu 690	ccc Pro	cag Gln	cta Leu	gtt Val 695	gca Ala	gct Ala	acc Thr	tcg Ser	aac Asn	cta Leu 700	cca Pro	ggg Gly	cca Pro	gca Ala	2112		
ccg Pro 705	ccc Pro	agt Ser	gaa Glu	ccg Pro	tgc Cys 710	gaa Glu	agc Ser	agc Ser	gca Ala	ttt Phe 715	ttt Phe	tac Tyr	cga Arg	cct Pro	gat Asp 720	2160		
ctg Leu	atc Ile	gtg Val	ctg Leu	ctg Leu 725	gtg Val	tcg Ser	ctg Leu	ctt Leu	acg Thr 730	gcg Ala	acc Thr	gtc Val	aga Arg	ttc Phe 735	ata Ile	2208		
caa Gln	taa															2214		

<210> 122
 <211> 737
 <212> PRT
 <213> Anopheles gambiae strain YAO

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 Pro Pro Ser Ala Leu Val Gln Gly Arg His His Glu Leu Asn Asn Gly
 35 40 45
 Ala Ala Ile Gly Ser His Gln Leu Ser Ala Ala Ala Gly Val Gly Leu
 50 55 60
 Ser Ser Gln Ser Ala Gln Ser Gly Ser Leu Ala Ser Gly Val Met Ser
 65 70 75 80
 Ser Val Pro Ala Ala Gly Ala Ser Ser Ser Ser Ser Ser Ser Leu Leu
 85 90 95
 Ser Ser Ser Ala Glu Asp Asp Val Ala Arg Ile Thr Leu Ser Lys Asp
 100 105 110
 Ala Asp Ala Phe Phe Thr Pro Tyr Ile Gly His Gly Glu Ser Ala Arg
 115 120 125
 Ile Ile Asp Ala Glu Leu Gly Thr Leu Glu His Val His Ser Gly Ala
 130 135 140
 Thr Pro Arg Arg Arg Gly Leu Thr Arg Arg Glu Ser Asn Ser Asp Ala
 145 150 155 160
 Asn Asp Asn Asp Pro Leu Val Val Asn Thr Asp Lys Gly Arg Ile Arg
 165 170 175
 Gly Ile Thr Val Asp Ala Pro Ser Gly Lys Lys Val Asp Val Trp Leu
 180 185 190
 Gly Ile Pro Tyr Ala Gln Pro Pro Val Gly Pro Leu Arg Phe Arg His
 195 200 205
 Pro Arg Pro Ala Glu Lys Trp Thr Gly Val Leu Asn Thr Thr Thr Pro
 210 215 220
 Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro
 225 230 235 240
 Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu
 245 250 255
 Tyr Ile Asn Val Val Ala Pro Arg Pro Arg Pro Lys Asn Ala Ala Val
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 275 280 285
 Asp Val Tyr Asp His Arg Ala Leu Ala Ser Glu Glu Asn Val Ile Val
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 Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu Phe Leu Gly
 305 310 315 320

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Gln	Ser	Gly	Ser	Pro	Thr	Ala	Pro	Trp	Ala	Leu	Val	Ser	Arg	Glu	Glu
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Ala	Thr	Leu	Arg	Ala	Leu	Arg	Leu	Ala	Glu	Ala	Val	Gly	Cys	Pro	His
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Glu	Pro	Ser	Lys	Leu	Ser	Asp	Ala	Val	Glu	Cys	Leu	Arg	Gly	Lys	Asp
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Asn	Pro	Asn	Pro	Asn	Thr	Ala	Ser	Ser	Glu	Phe	Pro	Glu	Trp	Pro	Lys
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His	Thr	Ala	His	Gly	Arg	His	Tyr	Leu	Glu	Leu	Gly	Leu	Asn	Thr	Ser
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Phe	Val	Gly	Arg	Gly	Pro	Arg	Leu	Arg	Gln	Cys	Ala	Phe	Trp	Lys	Lys
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Tyr Leu Pro Gln Leu Val Ala Ala Thr Ser Asn Leu Pro Gly Pro Ala
 690 695 700
 Pro Pro Ser Glu Pro Cys Glu Ser Ser Ala Phe Phe Tyr Arg Pro Asp
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 atg gtt ccg ctg ggt ctg ctc ggc gtg acc gcg ctg cta cta atc ctg 96
 Met Val Pro Leu Gly Leu Leu Gly Val Thr Ala Leu Leu Leu Ile Leu
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 Pro Pro Ser Ala Leu Val Gln Gly Arg His His Glu Leu Asn Asn Gly
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 gcc gcc atc gga tcg cat cag ctg tcg gct gcc gcc ggt gtt ggc ctt 192
 Ala Ala Ile Gly Ser His Gln Leu Ser Ala Ala Ala Gly Val Gly Leu
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 tcc tcc cag tcc gcc cag tcc gga tcg ctc gca tcc ggt gtg atg tca 240
 Ser Ser Gln Ser Ala Gln Ser Gly Ser Leu Ala Ser Gly Val Met Ser
 65 70 75 80

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Ser	Val	Pro	Ala	Ala	Gly	Ala	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Leu	Leu	
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Ser	Ser	Ser	Ala	Glu	Asp	Asp	Val	Ala	Arg	Ile	Thr	Leu	Ser	Lys	Asp	
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Ala	Asp	Ala	Phe	Phe	Thr	Pro	Tyr	Ile	Gly	His	Gly	Glu	Ser	Val	Arg	
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Ile	Ile	Asp	Ala	Glu	Leu	Gly	Thr	Leu	Glu	His	Val	His	Ser	Gly	Ala	
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Asp	Val	Tyr	Asp	His	Arg	Ala	Leu	Ala	Ser	Glu	Glu	Asn	Val	Ile	Val	
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cag Gln 385	agc Ser	ggc Gly	tcg Ser	ccg Pro	acg Thr 390	gca Ala	ccg Pro	tgg Trp	gca Ala	ttg Leu 395	gta Val	tcg Ser	cgc Arg	gag Glu	gaa Glu 400	1200
gcc Ala	acg Thr	cta Leu	aga Arg	gca Ala 405	ctg Leu	cgg Arg	ttg Leu	gcc Ala	gag Glu 410	gcg Ala	gtc Val	ggc Gly	tgc Cys	ccg Pro 415	cac His	1248
gaa Glu	ccg Pro	agc Ser	aag Lys 420	ctg Leu	agc Ser	gat Asp	gcg Ala	gtc Val 425	gag Glu	tgt Cys	ctg Leu	cgc Arg	ggc Gly 430	aag Lys	gat Asp	1296
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 Ala Ala Ile Gly Ser His Gln Leu Ser Ala Ala Ala Gly Val Gly Leu
 50 55 60
 Ser Ser Gln Ser Ala Gln Ser Gly Ser Leu Ala Ser Gly Val Met Ser
 65 70 75 80
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 85 90 95
 Ser Ser Ser Ala Glu Asp Asp Val Ala Arg Ile Thr Leu Ser Lys Asp
 100 105 110
 Ala Asp Ala Phe Phe Thr Pro Tyr Ile Gly His Gly Glu Ser Val Arg
 115 120 125
 Ile Ile Asp Ala Glu Leu Gly Thr Leu Glu His Val His Ser Gly Ala
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 Thr Pro Arg Arg Arg Gly Leu Thr Arg Arg Glu Ser Asn Ser Asp Ala
 145 150 155 160

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Asn Asp Asn Asp Pro Leu Val Val Asn Thr Asp Lys Gly Arg Ile Arg
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 Gly Ile Thr Val Asp Ala Pro Ser Gly Lys Lys Val Asp Val Trp Leu
 180 185 190
 Gly Ile Pro Tyr Ala Gln Pro Pro Val Gly Pro Leu Arg Phe Arg His
 195 200 205
 Pro Arg Pro Ala Glu Lys Trp Thr Gly Val Leu Asn Thr Thr Thr Pro
 210 215 220
 Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro
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 Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu
 245 250 255
 Tyr Ile Asn Val Val Ala Pro Arg Pro Arg Pro Lys Asn Ala Ala Val
 260 265 270
 Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala Thr Leu
 275 280 285
 Asp Val Tyr Asp His Arg Ala Leu Ala Ser Glu Glu Asn Val Ile Val
 290 295 300
 Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu Phe Leu Gly
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 325 330 335
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 Arg Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Val Ser Val Ser Leu
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 485 490 495
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 Leu Gln Ala Val Arg Glu Leu Asn Pro Tyr Val Asn Gly Ala Ala Arg
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 675 680 685
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